

## Sequence conservation and functional prediction

The results of sequence similarity searches are classified phylogenetically. "root-Haemophilus" indicates the best hit in the database after the self-alignment has been excluded. "Eubacteria-Proteobacteria" indicates the best hit to a protein from phylogenetically distant bacteria (those outside the Proteobacteria domain). The functional classification for each protein is given according to the 1-letter code that can be viewed under "Functional classification of genes/proteins"

Protein ortholog	E.coli	len	root	Score	Eubacteria	Score	Eukaryotae	Score	Function
			Haemophilus	-Proteobacteria					
F_HIN0001	cpdB	657	CNI6_ECOLI	2194	-	-	SNTD_BOVIN	73	2',3'-cyclic-nucleotide phos-
J_HIN0002	hncL	423	ATU23794_1	187	ANA_BACST	130	ATU23794_1	187	happuricase
S_HIN0003		279	ECOW67_156	107	-	-	-	-	
S_HIN0004		145	ECOW67_156	109	-	-	-	-	
S_HIN0005	pepe	226	PERE_SALTY	426	-	-	-	-	peptidase E
C_HIN0006		411	HYUC_PSESN	264	UN0885	260	-	-	N-carbamyl-L-amino acid am-
C_HIN0007		139	PHRPROE_4	111	-	-	-	-	oxidoreductase
E_HIN0008	potE	435	POTE_ECOLI	1756	BSU31756_2	105	A40775	72	putrescine-ornithine anti-
E_HIN0009	speF	720	DCOS_ECOLI	2484	DCOR_LACS3	1225	-	-	ornithine decarboxylase
R_HIN0010		509	ADP1_HUMAN	76	MLU15181_1	72	AQPI_HUMAN	76	permease
G_HIN0011	argI	310	ADP1_PSEAE	864	THPRPOB_1	60	CADB_XENLA	61	carbamate kinase
R_HIN0012	argI	334	OMPSCA	1453	MYCOTC_1	319	OTC_BANCA	241	ornithine carbamoyltransfer-
R_HIN0013	ylgI	272	S30716	241	YPPA_BACST	103	-	-	hydrolase
G_HIN0014	ybeI	160	YBEI_ECOLI	225	-	-	-	-	integral membrane protein
G_HIN0015		108	-	-	-	-	-	-	
L_HIN0016	oraA	126	RECX_ECOLI	95	-	-	-	-	regulator of RecA function
L_HIN0017	recA	354	ECRECA_1	1358	SVU04837_1	1117	ATHRECA_1	605	recA
S_HIN0018		217	-	-	-	-	-	-	
R_HIN0019	yjba	129	YJBA_ECOLI	282	-	-	-	-	membrane protein
H_HIN0020	henx	428	HEMX_ECOLI	642	-	-	-	-	uroporphyrinogen III cosynth
H_HIN0021	henx	332	HEMX_ECOLI	179	-	-	-	-	uroporphyrinogen III methyl
G_HIN0022	cyaa	843	CYAA_PASMO	891	-	-	-	-	adenylate cyclase
C_HIN0023	gpdA	335	GPD_A_ECOLI	1154	S41948	65	GPD_A_ECOLI	139	glycerol 3-phosphate dehydr
C_HIN0024	cyse	267	CYSE_ECOLI	998	SYOSRA_4	380	S52150	622	serine acetyltransferase
C_HIN0025	yglB	271	YJIB_ECOLI	137	-	-	Y46210	105	shikimate 5-dehydrogenase
R_HIN0026		461	YVH1_CAEEL	833	MLU15181_20	123	YVH1_CAEEL	263	cation transporter
H_HIN0027	fold	428	ECOW67_1	449	S48595	257	MTDC_MOUSE	388	5,10-methylene-tetrahydrofo.
C_HIN0028	fucP	216	FUCP_ECOLI	762	BMR2_BACU	62	-	-	L-fucose permease
G_HIN0029	fucA	144	FUCA_ECOLI	240	RBSD_BACU	76	HTS_DROME	92	fucose-1-phosphate aldola-
G_HIN0030	fucU	144	ECOW67_18	387	GNST_BACU	158	-	-	fucose transport protein
G_HIN0031	fucK	470	FUCK_ECOLI	240	RNTX_BACU	158	-	-	fucokinase
G_HIN0032	fucI	604	FUCI_ECOLI	1331	-	-	-	-	L-fucose isomerase

G_HIN0033	fucr	249	PFUCR_ECOLI	286	BACGMTZ_32	253	RGBHY1	65	L-fucose operon activator
I_HIN0034	hepa	923	HEPA_ECOLI	900	GRE_CLOAB	69	S39059	98	helicase
J_HIN0035	yabo	219	YABO_ECOLI	723	W302214_1	122	S50972	104	psuedoc synthetase
G_HIN0036	g1pr	192	ECOM67_349	340	-	-	-	73	glycerol metabolism protein
M_HIN0037	g1pr	255	GLPR_ECOLI	451	BACGMTZ_32	148	RHOM_DROME	-	glycerol-3-phosphate regulon
M_HIN0038	yaac	273	-	-	-	-	-	-	lipoprotein
R_HIN0039	yaeB	198	A43581	1287	-	-	-	-	permease
F_HIN0040	abc	345	YABE_ECOLI	458	BACOMPA_2	136	MDL2_YEAST	187	transport ATPase
K_HIN0041	yadB	164	YABD_ECOLI	733	GLNO_C_BACT	278	HIS1_PHYPR	67	hydrolyase (phosphatase)
J_HIN0042	def	169	DEF_ECOLI	423	YTDPEPM_2	80	-	-	methionylmethionylaminoacyl-L-
J_HIN0043	fmc	318	FMT_ECOLI	549	MSU10425_4	122	FTDH_RAT	198	methionyl-L-cRNA formyltransferase
J_HIN0044	fwv	451	ECOM67_213	324	S185529	89	A48998	121	rRNA methylase
P_HIN0045	trkA	458	TRKA_SALTY	1596	S26242	89	TRKA_METNA	228	TRK system potassium uptake
N_HIN0046	mscL	128	MSCL_ECOLI	399	CLOMSCL_1	193	DHE2_ACHIL	67	large mechanosensitive cond
E_HIN0047	ygfE	85	ECU28375_47	203	-	-	-	-	RNA polymerase sigma-E factor
L_HIN0048	rpoE	189	RPOE_SALTY	727	MLU15180_30	114	-	-	negative regulator of rpoE
L_HIN0049	mclA	195	MCLA_ECOLI	163	-	-	-	-	sigma factor negative regul
L_HIN0050	ccsA	315	PHRPOE_3	390	S27735	66	DEOK_HUMAN	65	patocarbonate kinase
H_HIN0051	ccsA	311	BVEKES	674	EFTU_BACPR	1552	EFLA_CANAL	154	translation elongation fact
S_HIN0052	tuftA	394	EFFECT	1904	-	-	-	-	nifH3-like regulator new A
S_HIN0053	yjbn	98	YADO_ECOLI	84	YACF_BACGU	90	S48817	103	transferrin-binding protein
L_HIN0054	lepa	327	YJBN_ECOLI	606	-	-	-	-	tryptophanyl-cRNA synthetase
S_HIN0055	lepa	933	YJBN_ECOLI	155	-	-	-	-	adenylosuccinate lyase
J_HIN0056	trpS	334	SYM_ECOLI	1378	SYM_BACST	367	SYMA_YEAST	342	ribosomal protein L10
S_HIN0057	ycfC	205	YCF_C_ECOLI	317	PUR8_BACGU	94	FUMH_HUMAN	98	UDP-n-acetylglucosamine pyr
F_HIN0058	pubB	456	YCF_C_ECOLI	1871	-	-	-	-	biothin sulfoxide reductase
J_HIN0059	trpJ	163	PUR8_ECOLI	497	R10_BACGU	238	ATU20183_1	80	cyclochrome C
J_HIN0061	trpJ	123	R5B810	370	R1A_HALEU	370	R1A_SCHPO	84	lysophospholipase
M_HIN0062	gluM	456	GLMU_ECOLI	1669	L1STMS_1	356	ATU22964_1	80	aspartate-semialdehyde dehy
C_HIN0063	bisc	825	TORC_ECOLI	929	YVAE_BACGU	105	FDMA_METRO	105	Mg2+-transporting ATPase
C_HIN0064	lecC	368	TORC_ECOLI	218	-	-	-	-	modulator of drug activity
C_HIN0065	plbB	313	P5BC12	135	S52201	72	CELK02P3_2	55	DNA helicase
I_HIN0066	aad	371	DHAS_ECOLI	704	DHAS_MYCMI	99	SPACSH10_5	588	1-lipopolysaccharide core bio
E_HIN0067	yjhd	238	SSU2024_2	99	SSU2024_2	99	-	-	3-deoxy-d-manno-octulosonic
M_HIN0068	mdaB	208	MAB_ECOLI	633	-	-	-	-	glycosyl transferase
L_HIN0069	repB	670	REP_ECOLI	1657	S27667	571	HUBYDH	140	DNA-3-methyladenine glycosyl
M_HIN0070	kabB	70	YBJM_ECOLI	60	SYOF1A_2	349	-	-	shikimate 5-dehydrogenase
M_HIN0071	kabB	156	KYTB_ECOLI	441	S28562	151	VAGT_TORCA	55	putative transcriptional reg
N_HIN0072	kabA	427	KOTA_ECOLI	914	YCOA_SYMP7	173	BAGT_MOUSE	62	zinc finger (DNA-binding ?) p
M_HIN0073	acac	254	YCOA_SYMP7	173	YCOA_SYMP7	173	-	-	transport ATPase
L_HIN0074	tag	185	3MG1_ECOLI	624	MLU15180_16	225	AR01_YEAST	90	transcription regulator
R_HIN0075	acac	272	AAOE_ECOLI	505	SPU11948_1	60	SUAS_YEAST	84	
R_HIN0076	ydcC	183	ECOM67_206	537	YMC_C_BACGU	127	ZG58_XENLA	51	
R_HIN0077	ydcD	178	ECOM67_207	308	TOP1_BACGU	129	CELFA2A10_5	474	
R_HIN0078	yhes	638	ECOM67_276	1256	TLRC_STRPR	228	CELFA2A10_5	474	
R_HIN0079	-	98	A41879	93	A47082	71	HSTAF1128_1	58	
R_HIN0080	-	119	HU32746	263	-	-	-	-	

P	HIN0081	993	S49087	198	-	-	-	transferrin-binding protein
K	HIN0082	581	CEPH11_3	354	SGDNACTRS_4	280	CEPH11_3	transport ATPase
R	HIN0083	552	HMT1_SCHPO	422	HEPA_ANASP	396	HMT1_SCHPO	transport ATPase
R	HIN0084	343	H1PA_ECOLI	75	-	-	-	h1pa protein, detected in v.
G	HIN0085	g1px	KENGLPX_1	1190	YMJ1_BACSU	593	-	glycerol metabolism (?) new
R	HIN0086	yiiu	YIIU_ECOLI	156	A43528	81	MYS3_HYDAT	myosin-like protein (coiled
R	HIN0087	mlac	MOC_ECOLI	398	CEXB_BACME	63	JN0458	flavodoxin-related protein
R	HIN0088	ylhz	YIHZ_ECOLI	403	S39374	335	-	new BCR
S	HIN0089	ydbb	YGBB_ECOLI	627	YACW_BACSU	502	-	new BCR
M	HIN0090	ydbp	ECU29579_44	278	YACW_BACSU	139	-	nucleotidyltransferase
S	HIN0091	ydbQ	ECU29579_45	193	-	-	-	xanthine-guanine phosphorib
F	HIN0092	155	XGPT_SALTU	318	HPRT_LACIA	62	XPA_HUMAN	X-his peptidase
F	HIN0093	pppd	JU0300	742	-	-	-	integrase-recombinase
G	HIN0094	xerc	C37841	889	CODV_BACSU	230	-	-
G	HIN0095	146	PSALMX	165	-	-	-	-
C	HIN0096	tpia	TPIS_ECOLI	795	TM0A_1	353	TPIS_PABIT	triosephosphate isomerase
G	HIN0097	glpe	BVEGGE	215	-	-	DIN1_FAPSA	sulfatase or Tyr phosphatase
R	HIN0098	rad	RAAD_ECOLI	164	YXXF_BACSU	65	-	membrane protein
E	HIN0099	ilvy	ILVY_ECOLI	637	M2509_1	223	-	transcription activator
E	HIN0100	ilvc	ISECKR	1898	A47037	162	S77495_1	ketol-acid reductoisomerase
C	HIN0101	glpc	GLPC_ECOLI	742	PER_PEPAS	70	S16351	anaerobic glycerol-3-phosph
C	HIN0102	glpb	GLPB_ECOLI	288	DNRP_STRPE	75	SGUT2A_1	anaerobic glycerol-3-phosph
C	HIN0103	glpa	DEBCNA	1959	U00022_1	135	GPDM_RAT	glycerol-3-phosphate permea
R	HIN0104	glpt	ECOMERT	448	GLPT_BACSU	400	MNMP11CT_1	permease
C	HIN0105	304	ECOMERT_6	68	YYAM_BACSU	64	NABA_RAT	glycerophosphoryl diester p
C	HIN0106	glpQ	GLPQ_ECOLI	1024	GLPQ_BACSU	161	CEK02C4_1	glycerol uptake facilitator
C	HIN0107	glpF	GLPF_SHEFL	1035	GLPF_BACSU	169	RATROP_1	glycerol kinase
F	HIN0108	glpk	KIRBGL	2111	GLPK_BACSU	1637	S46937	xanthine-guanine phosphorib
F	HIN0109	gpc	XGPT_SALTU	318	HPRT_LACIA	62	XPA_HUMAN	lipoprotein, acid phosphata
R	HIN0110	274	S37645_1	82	-	-	S37645_1	exopolyphosphatase
F	HIN0111	240	YPUL_BACSU	184	YPUL_BACSU	184	LD002459_1	coiled coil domain-containi
F	HIN0112	330	A45333	916	U00018_30	69	RTG2_YEAST	-
M	HIN0113	1298	YFFM_ECOLI	387	-	-	-	-
C	HIN0114	ylfm	YFFM_ECOLI	824	-	-	-	-
C	HIN0115	slpd	SLPD_ECOLI	638	S46228	79	CEU2C395_8	peptidyl-prolyl cis-trans i
S	HIN0116	yjpd	YJPD_SALTU	361	-	-	-	-
S	HIN0117	yjpb	ECU29579_42	583	-	-	-	-
R	HIN0118	yjbc	ECU29579_41	523	-	-	-	-
R	HIN0119	192	YIAB2_HABSO	806	S39339	63	-	acid phosphatase (?)
I	HIN0120	61	ECOMET_7_198	opt52	-	-	-	lipoprotein, alkaline phosp
I	HIN0121	nlpd	NLPD_ECOLI	488	XYLA_BACSU	93	-	-
I	HIN0122	mmts	MOTS_AZVT	2178	HEKA_STRPN	537	MSH2_HUMAN	lipoprotein
J	HIN0123	seia	S47812	1148	-	-	-	DNA repair protein, ATPase
J	HIN0124	seib	S47811	312	EFTL_STRRA	184	EFLA_YEAST	cysteiny1-tRNA (Ser) sele
J	HIN0125	re1b	REL1_ECOLI	75	-	-	-	translational elongation fac
P	HIN0126	102	RJ2PRP	59	-	-	-	negative regulator of trans
P	HIN0127	1084	S14548	173	JU07025_1	100	-	-
C	HIN0128	432	TIG_ECOLI	1449	MGU0177_1	79	YSC19324_6	transferrin-binding protein
								peptidyl-prolyl cis-trans i

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O	HIN0129	CLIP	193	CLPP_ECOLI	744	SSU16135.1	618	HSCCLPPMR.1	580	ATP-dependent Clp protease
C	HIN0130	clpx	411	A48709	1340	HSU1_BACU	142	YB77_YEAST	287	AMP-dependent protease AtPa
N	HIN0131	secc	106	SECE_ECOLI	210	SECE_THEMA	91	-	-	preprotein translocase subu
N	HIN0132	musg	185	NSUG_ECOLI	692	NSUG_BACU	372	R24P_SULO	54	transcription antiterminalo
R	HIN0133	vacj	250	VACJ_SHYEL	279	-	-	-	-	intercellular spread of Shi
O	HIN0134	yjgf	130	ECOW93.156	394	YABJ_BACU	227	YEO7_YEAST	171	new ACR
C	HIN0135	htpx	283	HPX_ECOLI	636	STAMEGRA.1	66	-	-	putative metalloprotease
R	HIN0136	yphp	93	YHHP_ECOLI	250	YVYE_BACU	175	HSPDUDOM.1	59	putative transcription regu.
S	HIN0137	lykx	206	YIGZ_ECOLI	533	YVYE_BACU	175	-	-	new BOR
P	HIN0138	trkx	423	TRKX_ECOLI	887	ENEMTP.11	68	SCMGTP4A.1	50	TRK system potassium uptake
S	HIN0139	yihl	186	YIHI_SALTY	155	-	-	-	-	-
S	HIN0140	-	-	-	-	-	-	-	-	-
P	HIN0141	lysp	208	ECOHU49.15	398	BACDEGSU.2	258	-	-	nitrate/nitrite response re
E	HIN0142	narA	415	DCDA_PSEBA	848	DCDA_BACU	231	DCOR_CAREL	114	diaminopimelate decarboxyla
L	HIN0143	recQ	649	EBECCQ	1629	YXIN_BACU	153	HUMDHQ1.1	302	DNA helicase
J	HIN0144	proS	572	STP_ECOLI	1068	STP_CHLIR	336	YER1_YEAST	302	prolyl-tRNA synthetase
U	HIN0145	ostA	782	YABG_ECOLI	329	ENP1_BACSH	73	-	-	endonucleidase(?)
R	HIN0146	-	127	ECU28377.11	197	-	-	-	-	periplasmic protein
S	HIN0147	-	50	-	-	-	-	-	-	-
C	HIN0148	sufI	311	ECU28377.11	434	SAPSHA.1	100	B48521	152	periplasmic protein, oxidore
C	HIN0149	plsc	240	PLSC_ECOLI	790	BORLSTGTD_	107	PLSC_YEAST	157	1-acyl-sn-glycerol-3-phosph
R	HIN0150	ydbf	237	YBDF_ECOLI	122	-	-	-	-	metalloprotease ?
E	HIN0151	llyg	508	NTG2_MOUSE	298	YBFA_BACU	58	NTG2_MOUSE	298	sodium-dependent amino acid
E	HIN0152	llyg	265	JQ0875	538	STMLIVACN.2	320	ILVA_PORUM	295	acetylacetic synthase II
E	HIN0153	llyv	612	DMECDA	2403	ILVD_CLOPA	377	SCXCSM83.2	331	dihydroxy-acid dehydratase
E	HIN0154	llyv	513	THD1_ECOLI	1417	THD1_BACU	265	THD1_LYCES	851	threonine dehydratase
L	HIN0155	dhaf	1159	VCU30472.2	3975	MG129.1	267	-	-	DNA polymerase III alpha su
G	HIN0156	ylfH	485	U00022.9	249	Y00022.9	249	SC8021X.4	186	phosphoglucomutase
S	HIN0157	ylfH	62	YTFH_ECOLI	105	YIFR_BACU	93	-	-	new BOR
S	HIN0158	ylfG	109	YTFG_ECOLI	130	-	-	-	-	-
N	HIN0159	secb	169	SECB_ECOLI	295	-	-	-	-	-
R	HIN0160	yibN	148	YIBN_ECOLI	371	MPLINRPHOM	61	HS6B_DROME	47	protein-export protein
X	HIN0161	ansB	349	U06943.1	1200	ASPG_BACLI	231	ASG2_YEAST	311	tyrosine phosphatase or sul
E	HIN0162	ndh	440	DCUB_ECOLI	469	NABD_BACU	78	YMD_YEAST	139	c4-dicarboxylate permease
C	HIN0163	plsb	444	PLSB_DECCR	759	-	-	-	-	NADH dehydrogenase
I	HIN0164	lexA	810	LEXA_PSEBU	1667	-	-	-	-	glycerol-3-phosphate acyltr
L	HIN0165	lexA	209	LEXA_PSEBU	604	U00019.5	186	-	-	SOS regulatory protein (rep
E	HIN0166	dapF	274	DAPF_ECOLI	1152	SS2295	181	-	-	diaminopimelate epimerase
O	HIN0167	-	165	TAGD_VIRCH	376	B43583	292	SP22_BOVIN	68	thiol antioxidant enzyme
F	HIN0168	purL	1320	PURL_ECOLI	2438	MLU15182.5	174	PUR4_YEAST	618	phosphoribosylformylglycina
S	HIN0169	-	382	YPCD_YEEN	477	-	-	-	-	-
G	HIN0170	-	303	S49339	109	BSU21332.1	76	S49339	109	L-glutamine-D-fructose-6-ph
S	HIN0171	yibQ	280	YIBQ_ECOLI	410	SYOCPCB.10	120	DDU07817.1	137	myosin-like protein
R	HIN0172	yibP	410	YIBP_ECOLI	413	S30866	120	-	-	phosphoglycerate mutase 1
C	HIN0173	gpmA	227	PMG1_ECOLI	652	MLU15186.19	590	PMBXY	617	50S ribosomal protein L31
J	HIN0174	rpmE	70	RJL1_ECOLI	288	MLU15186.19	129	-	-	-
L	HIN0175	mutY	378	MUTY_ECOLI	976	END3_BACU	101	-	-	A/g-specific adenine glyco
S	HIN0176	y95x	90	ECU28377.60	387	-	-	-	-	-

M	HINO177	Y9G2	357	ECU28377_62	581	-	LYG_ANSAN	47	lytic transglycosylase
M	HINO178	nadr	226				-		transcriptional regulator (
M	HINO179	ribB	421	NADR_SALT	837	MYCPSTICR_	128U YEAST	60	3,4-dihydroxy-2-butanone 4-1
R	HINO180	Y1BB	215	RIIB_ECOLI	731	GCH2_BACSU	S50973	228	glycosyl transferase
R	HINO181	Y1BK	282	PHU1958_2	200		-		rRNA methylase (spot family
S	HINO182	Y1BK	160	Y1BK_ECOLI	643	BCAPSAT_3			new ACR
S	HINO183	Y1BF	193	Y1BF_ECOLI	307	MTU00024_4	RNI18942_1	76	cell division, signal recog
M	HINO184	ftsE	414	FTSY_ECOLI	866	SMO4_BACST	SREC_ARATH	242	transport ATPase
M	HINO185	ftsE	218	FTSE_ECOLI	665	GNO_BACST	TAPL_HUMAN	96	cell division, membrane pro
M	HINO186	ftsX	310	FTSX_ECOLI	699		-		cell division, membrane pro
I	HINO187	Y9GF	393	529276	872	JC4032	JC2247	708	acetyl coenzyme A acetyltra
I	HINO188	acoA	243	acoB	1051		-		integral membrane protein
I	HINO189	acoA	223	PCAJ_BACSU	426	CPNA_CLOAB	A41771	217	3-oxoacyl CoA-transferase
E	HINO190	acoD	217	CPNA_CLOAB	611	YMBI_BACSU	A41771	283	3-oxoacyl CoA-transferase
E	HINO191	YPSJ	315	CYSB_ECOLI	143		-		transcription regulator
E	HINO192	YPSJ	118	RS10_ECOLI	504	S37489	RS20_HUMAN	80	30S ribosomal protein S10
J	HINO193	YPLC	208	YPLC_ECOLI	551	RL3_MYCCA	CELIC26E_7	132	50S ribosomal protein L3
J	HINO194	YPLD	200	RL4_YEPS	864	RL4_BACST	S50887	86	50S ribosomal protein L4
J	HINO195	YPLB	99	R5EC23	354	RL23_MYCA	S29999	117	50S ribosomal protein L23
J	HINO196	YPLB	273	RL2_YEPS	1298	BACRFL1_4	YBGO YEAST	222	ribosomal protein L2
J	HINO197	YPS	91	R3BC19	447	R3B519	RS15 YEAST	119	ribosomal protein S19
J	HINO198	YPLV	110	RL22_ECOLI	503	RL22_BACSU	RL17 YEAST	73	50S ribosomal protein L22
J	HINO199	YPS	235	R3BC3	1019	S10613	RS3 YEAST	71	ribosomal protein S3
J	HINO200	YPLP	136	RL16_ECOLI	632	RL16_BACSU	RM16 YEAST	106	50S ribosomal protein L16
J	HINO201	YPMC	63	JC2274	234	RL29_BACST	RL35 YEAST	67	50S ribosomal protein L29
J	HINO202	YPSQ	85	R3EC17	379	RS17_THEMA	RS11_XENTA	84	ribosomal protein S17
S	HINO203		201						
J	HINO204	YPLN	123	RL14_ECOLI	593	RL14_THEH	RL17 HUMAN	81	50S ribosomal protein L14
J	HINO205	YPLX	103	ECOM67_233	403	RL24_BACST	S51347	68	50S ribosomal protein L24
J	HINO206	YPLX	179	ECOM67_232	845	RL5_BACST	RL5 HALMA	125	50S ribosomal protein L5
J	HINO207	YPSH	101	ECOM67_231	473	RBS14	CEIO1E8_4	111	30S ribosomal protein S14
J	HINO208	YPSH	130	ECOM67_230	562	RS8 MYCCA	RS1A STRPU	57	30S ribosomal protein S8
J	HINO209	YPLF	177	JC2281	705	BACGB_1	RL6 METVA	67	50S ribosomal protein L6
J	HINO210	YPLR	117	RL18_ECOLI	497	RL18_BACST	RL18 HALMA	62	50S ribosomal protein L18
J	HINO211	YPSB	166	ECOM67_227	768	RS5_BACST	RS4 YEAST	107	50S ribosomal protein S5
J	HINO212	YPMU	59	JC2284	242	RL30_BACST	RL30 HALMA	63	50S ribosomal protein L30
J	HINO213	YPLD	144	RL15_ECOLI	602	RL15_MYCCA	RL15 METVA	82	50S ribosomal protein L15
N	HINO214	YSEC	441	SECY_ECOLI	1181	SECY_STYR	SECY HALMA	64	50S ribosomal protein L15
J	HINO215	YPMU	37	RL36_ORSEA	146	RL6_CULTR			50S ribosomal protein L36
J	HINO216	YPSM	122	R3EC13	487	RBS13	S50886	81	ribosomal protein S13
J	HINO217	YPSK	129	R3EC11	629	RS11_BACSU	RS14 TRYB	103	ribosomal protein S11
J	HINO218	YPSD	206	R3BC4	942	A37146	RS11 YEAST	95	ribosomal protein S4
J	HINO219	YPLA	328	RPOA_ECOLI	795	RPOA_BACSU	REOA FYRSA	215	DNA-directed RNA polymerase
J	HINO220	YPLD	158	RL17_ECOLI	570	F32307	RM08 YEAST	137	50S ribosomal protein L17
G	HINO221	asIB	129	PDUI7435_1	90	NICA_AMASP	KAPR_BIAMM	70	transcription regulator (cm
R	HINO222		241	CHUR_BACTN	294	CHUR_BACTN			arylsulfatase regulatory pr
R	HINO223		268	HTU33772_5	80				permease
R	HINO224	yaem	397	yaem	143	-	-	-	ATP-binding protein

J	HIN0225	frt	185	REP_ECOLI	655	STRDNORF_1	62	NUP_DAUCA	365	ribosome releasing factor
G	HIN0226	pckA	538	ECOWM67_327	1948	STRPEPCK_1	644	U09241_1	737	phosphoenolpyruvate carboxyl
E	HIN0227	yrtI	293	ECOWM67_325	776	YACB_BACU	81	-	-	new BCR
E	HIN0228	argH	457	ABLY_ECOLI	1730	SCARGH_2	93	S32580	802	argininosuccinate lyase
F	HIN0229	galU	295	GTAB_BACU	809	GTAB_BACU	281	E28E_YEAST	102	glucosephosphate uridylyltransferase
G	HIN0230	csrA	63	ERMRSMA_1	221	CSR_A_BACU	160	-	-	carbon storage regulator
J	HIN0231	alas	874	SYA_ECOLI	3198	MCO47_1	262	SYAC_YEAST	231	alanyl-tRNA synthetase
K	HIN0232	uspa	141	S47715	513	YXIE_BACU	78	-	-	universal stress protein
E	HIN0233	pepP	430	DPECP	950	JN0491	200	PEPD_HUMAN	266	X-Pro aminopeptidase
G	HIN0234	ygtB	182	YGBB_ECOLI	257	-	-	-	-	aldose 1-epimerase precursor
G	HIN0235	galM	340	GALM_ECOLI	220	MURO_LACIB	105	HSU11036_1	120	galactokinase
G	HIN0236	galK	397	KIECGG	448	GAL1_LACIB	232	GAI2_HUMAN	105	galactose-1-phosphate uridylyltransferase
G	HIN0237	galT	349	KNECDG	1362	GAL7_STRL1	191	A4473	891	galactose operon repressor
C	HIN0238	galS	332	ECOH47_42	932	CGR_A_BACU	283	-	-	D-galactose-binding protein
G	HIN0239	mgjB	349	DEAL_CITFR	897	TR38_TREPA	106	-	-	D-galactose-binding protein
G	HIN0240	mgjA	506	WOLA_ECOLI	1920	RSB_BACU	380	DROOPSB5_1	61	galactoside transport ATPase
R	HIN0241	mgjC	336	MOIC_ECOLI	1389	RBSB_BACU	321	ABEC2_MOUSE	136	galactoside permease
R	HIN0242	-	244	CEN01FL_5	61	-	-	CEN01FL_5	61	membrane protein
R	HIN0243	yciB	185	ECU24203_3	442	-	-	-	-	integral membrane protein
R	HIN0244	yciA	154	YC1A_ECOLI	477	-	-	-	-	-
Z	HIN0245	yciI	98	YC1I_ECOLI	330	-	-	-	-	-
E	HIN0246	sic	593	SLT_ECOLI	259	-	-	-	-	-
M	HIN0247	trpR	101	TRPR_ENTAE	183	-	-	-	-	-
M	HIN0248	ytdM	194	ECOWM67_137	584	PBPB_BACU	289	-	-	-
C	HIN0249	fidC	114	FRDD_ECOLI	224	-	-	-	-	-
C	HIN0250	fidB	132	FRDC_PROVU	196	PHAG_FRBDI	52	MTCCGNS_2	153	soluble lytic murein transglucosylase
C	HIN0251	fidA	256	RDCRS	521	U00022_19	207	AA2732	300	tryptophan repressor
J	HIN0252	yleA	559	FDA_PROVU	1429	U00022_18	262	-	-	tryptophan repressor
J	HIN0253	yleB	333	ECOWM67_70	600	STK_BACU	215	SYKC_YEAST	175	penicillin-binding protein
G	HIN0254	cpxR	227	CXPR_ECOLI	404	YCBL_BACU	227	-	-	penicillin-binding protein
S	HIN0255	smuA	189	SMUA_ECOLI	98	-	-	-	-	penicillin-binding protein
S	HIN0256	yleK	341	YBK_ECOLI	833	-	-	-	-	penicillin-binding protein
S	HIN0257	yleJ	72	YELJ_ECOLI	172	-	-	-	-	penicillin-binding protein
R	HIN0258	yleM	585	YELM_ECOLI	621	-	-	-	-	penicillin-binding protein
L	HIN0259	coda	276	CODA_ECOLI	91	-	-	-	-	penicillin-binding protein
S	HIN0260	-	45	-	-	-	-	-	-	penicillin-binding protein
H	HIN0261	mob	192	MOB_ECOLI	267	-	-	-	-	penicillin-binding protein
S	HIN0262	yihD	88	YIHD_ECOLI	301	-	-	-	-	penicillin-binding protein
O	HIN0263	dsbA	205	ECDSBA_1	288	LP15278_1	58	CHKP4HB02_1	54	thiol:disulfide isomerase
S	HIN0264	yleB	111	YIEB_ECOLI	327	-	-	-	-	thiol:disulfide isomerase
J	HIN0265	trmA	363	TRMA_ECOLI	1240	S41759	67	RNOL_YEAST	102	tRNA (uracil-5-)-methyltransferase
C	HIN0266	yhiQ	257	S47717	726	-	-	-	-	tRNA (uracil-5-)-methyltransferase
C	HIN0267	-	144	-	-	-	-	-	-	tRNA (uracil-5-)-methyltransferase
R	HIN0268	yihC	178	PHRPOB_4	119	RSDNTHAB_4	68	CEIC25B6_4	66	ferredoxin-like oxidoreductase
R	HIN0269	yieO	463	YIEO_ECOLI	265	SPDNATR_1	241	YK85_YEAST	172	ferredoxin-like oxidoreductase
E	HIN0270	dpdA	253	DPPA_ECOLI	1370	APPA_BACU	131	-	-	ferredoxin-like oxidoreductase
S	HIN0271	-	253	-	-	-	-	-	-	ferredoxin-like oxidoreductase
S	HIN0272	yhan	115	YHAN_ECOLI	246	-	-	-	-	ferredoxin-like oxidoreductase

L	HIN0273	polA	930	DP01_ECOLI	1440	THP0LA_1	711	-	DNA polymerase I
S	HIN0272	ygfE	100	ECU28377_9	156	-	-	-	5-formyltetrahydrofolate cy
S	HIN0271	ygfA	187	YGF_A_ECOLI	465	SS1716	77	PTHG_RABIT	ADP-dependent ClpB protease
O	HIN0276	clpB	856	CLP_B_ECOLI	3001	SSU20646_1	1342	H101_ARATH	rRNA methylase (spou family
J	HIN0277	yjH	246	YJH_ECOLI	576	YAOO_ECOLI	212	S4881	exoribonuclease
L	HIN0278	vabB	782	VAB_B_ECOLI	1701	S46946	200	CELFA8E8_1	
S	HIN0279	ybhO	235	YBH_O_ECOLI	583	-	-	-	
S	HIN0280	pakH	229	B43361	342	STCFPR_A_1	125	CEL57B9_10	pyridoxamine-phosphate oxid
R	HIN0281	yjHk	616	YJH_K_ECOLI	2415	SI8572	243	Y081_CAEEL	GTPase
Z	HIN0282	glnA	472	GLN_A_PROCVI	1792	GLN_A_SYND2	962	FLUG_EMENI	glutamate--ammonia lyase
M	HIN0283	-	247	CLD1_ECOLI	106	-	-	-	lipopolysaccharide chain lei
M	HIN0284	-	404	S30030	88	-	-	-	putative o-antigen transpor
M	HIN0285	-	250	ECKFAAF_2	241	BSU13979_2	146	DPM1_YEAST	glycosyl transferase
S	HIN0286	-	185	EAAMAS1_5	68	-	-	-	glycosyl transferase
S	HIN0287	-	34	-	-	-	-	-	
M	HIN0288	-	306	ECONESK92_1	opt104	-	-	-	glycosyl transferase
M	HIN0289	-	471	EAAMAS1_1	1383	SS2736	251	-	undecaprenyl-phosphate gala
N	HIN0290	rffE	338	NGCOP3_2	1192	SP62_BACSU	432	GALX_YEAST	up-n-acetylglucosamine epi
F	HIN0291	-	399	EXOO_RHIME	82	-	-	-	exopolysaccharide productio
F	HIN0292	-	507	AMPA_ECOLI	266	MYCAMNO_1	204	ABPOL	amphopelidase A/I
F	HIN0293	ndk	141	NDK_ECOLI	433	MDK_BACSU	359	BMT18906_1	nucleoside diphosphate kin
R	HIN0294	ybhZ	390	YBH_Z_ECOLI	1554	OBG_BACSU	836	YHM8_YEAST	membrane protein
R	HIN0295	ybhE	307	YBH_E_ECOLI	556	YVAM_BACSU	90	-	50S ribosomal protein l27
J	HIN0296	xpmA	85	R5EC27	371	RL27_BACSU	232	RL27_TOBAC	50S ribosomal protein l21
J	HIN0297	rplU	103	RL21_ECOLI	421	RL21_BACSU	149	-	geranylgeranyl pyrophosphat
S	HIN0298	ispB	329	ISP_B_ECOLI	1082	GRC3_BACSU	406	GAPP_NEUCR	
S	HIN0299	-	245	-	-	-	-	-	
F	HIN0300	-	456	DAGA_ALTHA	404	YXA_BACSU	99	GAP1_YEAST	alanine permease
O	HIN0301	arcA	226	ARCA_ECOLI	515	R6SD_ECOLI	292	OMPR_PORAB	aerobic respiration control
C	HIN0302	dsbD	579	ECOW93_51	787	THIO_BACSU	53	THIO_CAEEL	thiol:disulfide isomerase
R	HIN0303	-	134	HU12834_4	58	-	-	-	membrane protein
F	HIN0304	purH	532	PUR_ECOLI	1308	PUR9_BACSU	351	PUR9_CHICK	phosphoribosylamimidazole'
F	HIN0305	purD	429	PUR2_SALTY	1505	PUR2_BACSU	450	S37104	phosphoribosylamine--glycin
F	HIN0306	glaY	421	GLA_Y_ECOLI	1603	GLA_Y_BACSU	692	GLYC_YEAST	serine hydroxymethyltransfe
R	HIN0307	yacB	206	YAC_ECOLI	440	S49524	187	HSU18919_1	ATPase
R	HIN0308	yacG	68	YAC_G_ECOLI	145	-	-	-	Zn finger protein
L	HIN0309	rlbB	418	RLB_B_ECOLI	1263	YX1N_BACSU	360	S42639	RNA helicase
R	HIN0310	-	187	BM3B_BACME	112	BM3B_BACME	112	-	transcriptional regulator
R	HIN0311	-	414	S39629	160	SSP5_STRGA	82	-	permease
R	HIN0312	-	1032	S39630	344	BNCBMAX_1	156	SS2525	cell division protein
M	HIN0313	ftsN	204	FTSN_ECOLI	116	-	-	-	multifunctional resistance protei
N	HIN0314	emrB	510	EMR_B_ECOLI	1840	TCNA_STRGA	330	SCDNAGERS_8	multifunctional resistance protei
N	HIN0315	emrA	350	EMR_A_ECOLI	889	-	-	-	glutamate 5-kinase
H	HIN0316	fofA	160	DVRA_ECOLI	435	DYRB_STANU	196	DRT2_ARATH	glutamate 5-kinase
E	HIN0317	proB	368	PROB_SEMA	863	THPPOB_1	398	YHU3_YEAST	pyruvate-related pyrophosphoryl
R	HIN0318	ygpB	196	ECU29581_42	687	MSGDWA_9	81	YSCP5U1A_1	permease
R	HIN0319	-	264	PROARA	74	-	-	-	prolipoprotein diacylglycer
I	HIN0320	lgt	268	LGT_ECOLI	534	-	-	-	

H	HIN0321	thyA	283	SYB5TB	211	S35239	210	TYSY_HUMAN	172	thymidylate synthetase
H	HIN0322	ythC	173	YTHC_ECOLI	383	YAAJ_BACCU	267	S53395	107	CMP (dCMP) deaminase
S	HIN0323		104	-						
S	HIN0324		100	-						
S	HIN0325	seca	901	SECA_ECOLI	3084	SECA_BACCU	686	-		preprotein translocase, put.
L	HIN0326	mutT	136	MUTT_ECOLI	337	MUTX_STRN	71	80DP_HUMAN	72	mutator (Aar-GC transversion)
L	HIN0327	kefC	618	KEFC_ECOLI	510	LIDP2_1	119	YJ90_YEAST	62	glutathione-dependent Na/H ;
R	HIN0328		254	ABD1_YEAST	89	B48290	83	ABD1_YEAST	89	SAM-dependent methyltransfe.
J	HIN0329	rpsB	251	R3C2	1012	R82_SPIPL	878	A54012	121	ribosomal protein S2
J	HIN0330	tsf	283	EFPS	586	EFTS_SPIPL	254	HBS1_YEAST	67	translation elongation fact.
I	HIN0331	lpxD	341	S47742	1478	CARG_STAAU	92	HSU23028_1	88	UDP-3-O-(R-3-hydroxymyristo)
M	HIN0332	hlpA	197	S47341	540	M49_STRPY	77	KATA_ARATH	90	histone-like membrane protei
M	HIN0333		795	S47340	186	-				outer membrane protein
R	HIN0334	yael	443	YAEI_ECOLI	355					Zn protease
R	HIN0335	cdsA	288	CDSA_ECOLI	343	MGU02189_1	64	YBN9_YEAST	81	CDP-diacylglyceride synthetase
R	HIN0336		239	Y065_MYCLE	459	Y065_MYCLE	459	SC6543_8	163	membrane protein; new ACR
J	HIN0337	lps	861	SYL_ECOLI	3347	SYL_BACCU	450	D21851_1	515	leucyl-tRNA synthetase
M	HIN0338	rlpB	182	RLPB_ECOLI	172					rare lipoprotein B
J	HIN0339	hola	344	HOLA_ECOLI	342					DNA polymerase III delta sub
J	HIN0340	glyS	688	S47780	2256	CTU20547_1	134			glycine-tRNA synthetase bet.
S	HIN0341		121	HTU3796_3	140					
S	HIN0342		86							
J	HIN0343	glyY	302	SYGA_ECOLI	1465	CTU20547_1	625			glycyl-tRNA synthetase alpha
C	HIN0344		508	BFU18676_1	1899	BFU18676_1	1899	S49465	1510	catalase
R	HIN0345	ygic	393	YGIC_ECOLI	218					glutathionylspermidine synt
S	HIN0346		206							
S	HIN0347		161							
C	HIN0348	eno	436	ECU29580_4	1098	ENO_BACCU	983	MCU09194_1	416	enolase
C	HIN0349	yhjN	401	YHJN_ECOLI	538	SATFP2_2	79	CET06H1_1	79	dehydrogenase
C	HIN0350	nrfG	384	NRFI_ECOLI	328			YSC19677_4	89	cytochrome c biogenesis pro
C	HIN0351		176	YEOJ_ECOLI	223	U00018_5	86	S45488	73	thioredoxin
C	HIN0352	nrfE	635	S49616	869	U00018_1	94			cytochrome c biogenesis pro
N	HIN0353	subB	267	SUBH_ECOLI	889	MU15181_9	159	MYOP_HUMAN	164	inositol monophosphatase
N	HIN0354		170	FMAA_BACNO	76	CMG3_BACCU	66			pilin
N	HIN0355		238	PPDE_ECOLI	82					general secretion protein
N	HIN0356		227							
N	HIN0357		101	GSPI_ERWCA	69					general secretion protein
L	HIN0358	recC	1121	EX5C_ECOLI	528	SYORP51_1	291			exodeoxyribonuclease V, nuc.
L	HIN0359	ybad	149	YBAD_ECOLI	548					Zn finger protein
H	HIN0360	ribD	370	RIBG_ECOLI	833	RIBG_BACCU	540	RIB7_YEAST	111	riboflavin biosynthesis pro
O	HIN0361	hobB	340	HOB_ECOLI	336	MU15180_31	93	ZOI_MOUSE	82	membrane protease
I	HIN0362	mutM	271	FPE_ECOLI	822	FPG_BACFI	293			formamidoypyrimidine-DNA gly
E	HIN0363		511	ACCT249D_1	1870	SPGADAGM_1	88	PIG6AD67B_1	272	glutamate decarboxylase
R	HIN0364		132	B49205	184					virulence-associated protein
R	HIN0365		77	YPFI_ECOLI	134					virulence-associated protein
R	HIN0366	ysjG	454	JCI497	S44189		334	OAT_VITAC	184	amino transferase
J	HIN0367	rpmG	56	S44444	231	RLJ3_BACST	95			ribosomal protein L33
J	HIN0368	rpmB	78	S42443	360	RL28_BACCU	108	S50921	102	ribosomal protein L28



L_HIN0369	radC	234	RADC_ECOLI	562	RDC_H_BACSU	345	-	DNA repair protein
L_HIN0370	dtp	400	DTP_ECOLI	905	BDP_STAB	129	SIS2_YEAST	pantothenate metabolism flar
L_HIN0371	dat	151	DUT_ECOLI	628	MLU0151_13	71	DUT_LYC8S	deoxyribitol triphosphate
L_HIN0372	tkk	218	TTK_ECOLI	628	S18996	92	-	transcription regulator
S_HIN0373	yheU	56	ECOW67_278	132	-	71	-	-
G_HIN0374	crp	224	CRP_ECOLI	851	NTCA_ANAPB	75	CEG3OD1_1_2	catabolite gene activator
R_HIN0375	-	392	ECU29560_10	97	SARLPPO_2	55	-	SM-dependent methyltransferase
R_HIN0376	-	351	AUTCH60_1	153	YZBA_BACSU	121	-	glycosidase
R_HIN0377	-	130	YHT_SYNF7	208	YHT_SYNF7	208	BTU09405_1	Zn-binding protein
J_HIN0378	11eS	941	SYEIT	2503	SVI_STAU7	568	SVY_NEUCR	isoleucyl-tRNA synthetase
R_HIN0379	YaeC	312	YAC_ECOLI	396	CORFDS_1	170	-	nucleotidyltransferase
R_HIN0380	-	510	WYIN_SALTY	465	MSGDAB_12	81	-	permease
J_HIN0381	rpsT	87	S40547	322	RS20_BACSU	73	-	30S ribosomal protein S20
S_HIN0382	-	188	-	-	-	-	-	-
S_HIN0383	-	34	-	-	-	-	-	-
H_HIN0384	menB	285	MENB_ECOLI	1347	MENB_BACSU	735	ECWH_RAT	naphthoate synthase
H_HIN0385	menC	347	MENC_ECOLI	414	-	-	-	o-succinylbenzoate-CoA synth
E_HIN0386	-	149	ACNARQ_1	509	AROD_MYCTU	295	A26020	3-dehydroquinate
E_HIN0387	accB	155	BCBP_ECOLI	352	ANARCB_2	214	ATTS1191_1	biotin carboxyl carrier pro
I_HIN0388	accC	448	ACCC_ECOLI	1961	ACCC_ANAPB	592	TOBBCSO_1	biotin carboxylase
S_HIN0389	-	289	S27484	772	-	-	-	transferrin-binding protein
S_HIN0390	-	481	HU32780_7	415	-	-	-	-
S_HIN0391	yndT	85	ECOW67_187	187	-	-	-	-
R_HIN0392	panF	484	ECOW67_188	1608	SAU06451_1	142	NACG_RABIT	pantothenate permease
R_HIN0393	-	128	YTRI_BUCAP	73	YVAM_BACSU	71	CELCS4A12_2	integral membrane protein
R_HIN0394	-	170	YVPM_BACSU	119	YVPM_BACSU	119	-	cell filamentation protein
M_HIN0395	fic	191	ECOPABA_3	70	-	-	-	permease
R_HIN0396	prna	296	PRNA_ECOLI	836	S41759	274	ODP1_YEAST	ribosomal protein L11 methy
R_HIN0397	yhdG	330	YHDG_SALTY	1103	YACF_BACSU	466	YQ12_CAMEL	nifR3-like nitrogen regulat
L_HIN0398	fis	99	pdB_1F1A	398	C1OACR_1	86	-	Hin recombinational enhance
S_HIN0399	smpB	161	SMPB_ECOLI	660	AA3259	179	-	new BCR
G_HIN0400	pfkA	321	K6P1_ECOLI	784	K6PF_BACST	592	K6P1_YEAST	phosphofructokinase
S_HIN401	-	193	HU18657_4	1014	-	-	-	-
S_HIN402	yaaA	272	YAAA_ECOLI	822	-	-	-	-
R_HIN403	smf	373	SMF_ECOLI	607	SMF_BACSU	228	-	gene required for DNA uptak
E_HIN404	1eua	531	RPLPA_5	1668	LEU1_LACIA	817	SOYSJANA_1	isopropylmalate synthase
E_HIN405	1eub	358	LEU3_SALTY	1347	LEU3_LEPIN	675	LEU3_BRANA	3-isopropylmalate dehydroge
E_HIN406	1euc	469	S40586	1484	LEU2_LACIA	511	LEU2_RHRA	3-isopropylmalate dehydrata
E_HIN407	leuB	200	LEUB_SALTY	773	LEUB_LACIA	233	USMLEU1A_1	3-isopropylmalate dehydrata
R_HIN408	-	1694	NMG1AP1_1	942	-	-	-	Igal1 protease
L_HIN409	recF	359	RBCF_ACEPL	1332	RBCF_STRCO	174	A54817	repeat ATPase
L_HIN410	dnaN	366	DNAN_ECOLI	1206	S77055_2	281	-	DNA polymerase III beta sub
L_HIN411	dnaA	454	DNA_A_ECOLI	1015	DNA_A_BACU	583	CC18_SCHPO	chromosomal replication inh
L_HIN412	-	912	TB12_NEIME	735	-	-	-	transferrin-binding protein
P_HIN413	-	625	TB21_NEIME	176	-	-	-	transferrin-binding protein
S_HIN414	-	481	HU32778_4	981	-	-	-	-
J_HIN415	rpmH	44	R134_ECOLI	192	R134_BACST	172	S52680	50S ribosomal protein L34
L_HIN416	rnpA	119	RNP1_ECOLI	420	BSRNP1PO_1	83	-	RNase P protein component

S	HIN0417	yJdd	86	YNP_PROMI	294	-	-	HSOXA_HS_1	77	inner membrane protein
E	HIN0416	yJdc	541	60TM_ECOLI	1052	MSGDAB_21	186	HSOXA_HS_1	179	Grpase
R	HIN0419	YJdf	461	THDF_ECOLI	1689	THDF_BACSU	294	WST1_YEAST	99	peptidyl-prolyl cis-trans isomerase
R	HIN0420	PSA	594	PSA_BACSU	126	PSA_BACSU	126	SS2764		peptidyl-prolyl cis-trans isomerase
R	HIN0421	yJ9x	519	YOGX_ECOLI	240	-	-	-		lipoprotein signal peptidase
M	HIN0422	1p9A	171	LSBP_ECOLI	430	LSBP_STYAU	156	-		involved in penicillin tolerance
M	HIN0423	yJfB	314	LYTB_ECOLI	1119	-	-	HUMOB1A_1	88	competence locus, DNA-binding
E	HIN0424	yJbI	112	CHE1_BACSU	111	CHE1_BACSU	111	D3H1_RAT	166	transcription regulator
R	HIN0425	yJbJ	256	ECU29579_32	1045	S48604	123	-		dehydrogenase
S	HIN0426	yJbK	301	ECU29579_33	643	-	-	-		aldolase
S	HIN0427	yJbK	413	ECU29579_34	710	-	-	-		sugar isomerase or lyase
R	HIN0428	yJbL	210	ECU29579_35	603	-	-	RNAADNCHT_1	61	4-hydroxybutyrate dehydrogenase
G	HIN0429	yJbM	258	ECU29579_36	851	YXDH_BACSU	66	CELC05D11_2	383	permease
C	HIN0430	-	315	APAGED_3	647	CAP1_STYAU	69	ATD18MR_1	65	permease
E	HIN0431	-	488	GNTF_BACSU	360	GNTF_BACSU	360	-		permease
C	HIN0432	-	142	-	-	-	-	-		permease
C	HIN0433	-	219	SFU12567_2	367	SFU12567_2	367	NAU20490_1	113	glycerol uptake facilitator
R	HIN0434	-	35	-	-	-	-	-		161016-V6 insertion element
R	HIN0435	tbpA	332	TBPA_ECOLI	532	-	-	CIN1_RAT	56	thiamin-binding periplasmic
R	HIN0436	yJbK	538	YABK_ECOLI	1020	CYSW_STYU7	103	-		permease
R	HIN0437	yJbJ	215	YABJ_ECOLI	547	MSBK_STYU	350	MDP5_DROME	109	transport ATPase
H	HIN0438	bJbB	333	BIOB_SEMMA	1005	U00010_21	1254	ATISECA_1	534	biotin synthetase
G	HIN0439	CKbB	665	TKT2_ECOLI	1547	U00013_20	343	TKT2_YEAST	339	transketolase 2
R	HIN0440	-	225	YTFV_ECOLI	257	YCKG_BACSU	170	-		periplasmic binding protein
G	HIN0441	yJAS	231	YIAS_ECOLI	913	-	-	MAG_DERPA	64	L-ribulose-phosphate 4-epimerase
C	HIN0442	yJAS	286	YIAR_ECOLI	1036	-	-	-		periplasmic
C	HIN0443	xyJk	485	XYJK_ECOLI	1338	BACKTAB_4	173	SS2675	110	xylose kinase
R	HIN0444	yJAO	328	YIAO_ECOLI	931	-	-	-		periplasmic solute-binding protein
R	HIN0445	yJAO	425	YIAO_ECOLI	1420	BPTIMBC_6	231	P_HUMAN	83	permease
R	HIN0446	yJAM	161	YIAM_ECOLI	275	-	-	-		integral membrane protein
C	HIN0447	yJAK	332	YIAK_ECOLI	1327	-	-	MDH_METPE	206	dehydrogenase
C	HIN0448	yJAJ	268	YIAJ_ECOLI	586	GYLR_STIRO	112	-		transcriptional regulator
E	HIN0449	serB	314	SRRB_ECOLI	754	YPPA_BACST	87	SRRB_YEAST	189	phosphoserine phosphatase
S	HIN0450	-	163	VA017054	252	-	-	-		permease
P	HIN0451	CORA	315	CORA_SALTY	1108	YQXL_BACSU	156	-		Mg2+ transport protein
R	HIN0452	yJ9T	181	ECU28377_50	221	-	-	-		integral membrane protein
F	HIN0453	-	294	SOYGPAFR_1	84	PURL_LACCA	69	SOYGPAFR_1	84	amido-phosphoribosyltransferase
R	HIN0454	-	400	S33279	61	-	-	S33279	61	NTP-utilizing enzyme
I	HIN0455	-	334	T2D1_HERAU	248	T2D1_HERAU	248	PMY1_SCHRO	80	restriction endonuclease
E	HIN0456	metH	304	MTD1_HERAU	698	MTD1_HERAU	698	PMY1_SCHRO	80	site-specific DNA methyltransferase
C	HIN0457	-	617	ECOWM89_66	622	U00017_27	198	CSR03D7_1	475	methionine synthase
C	HIN0458	-	166	YOGX_ECOLI	41	NMDM_SYNY3	78	G30315	124	ferredoxin
C	HIN0459	-	203	TORD_ECOLI	88	-	-	-		putative B type cytochrome
C	HIN0460	dmsC	279	DMS_C_ECOLI	275	-	-	SC6652X		

inner membrane protein  
Grp94  
peptidyl-prolyl cis-trans isomerase  
membrane-bound metal peptidase  
lipoprotein signal peptidase  
involved in penicillin tolerance  
competence locus, DNA-binding  
transcription regulator  
dehydrogenase  
aldolase  
sugar isomerase or lyase  
4-hydroxybutyrate dehydrogenase  
permease  
glycerol uptake facilitator  
IS1016-V6 insertion element  
ethanol-binding periplasmic  
permease  
transport ATPase  
biotin synthetase  
transketolase 2  
periplasmic binding protein  
L-ribulose-phosphate 4-epimerase  
xylose kinase  
periplasmic solute-binding protein  
permease  
integral membrane protein  
dehydrogenase  
transcriptional regulator  
phosphoserine phosphatase  
Mg<sup>2+</sup> transport protein  
integral membrane protein  
amido-phosphoryl transfer  
NTP-utilizing enzyme  
restriction endonuclease  
site-specific DNA methyltransferase  
methionine synthase  
ferredoxin  
putative B type cytochrome  
anaerobic dimethyl sulfoxide  
dimethylsulfoxide reductase  
anaerobic dimethylsulfoxide  
mercury transport protein

P_HIN0465	92	S18588	88	-	AT7A_HUMAN	82	mercury scavenger protein
P_HIN0466	614	SCMSMDRIA_1	383	-	SCMSMDRIA_1	383	transp. ATPase
P_HIN0467	288	ARAL_STRLT	160	ARAL_STRLT	-	-	Arac-like transcription regn
S_HIN0468	113	YAC7_ALCEU	171	B26872	102	-	new BCR
S_HIN0469	460	-	-	-	-	-	-
L_HIN0470	505	T3RE_BPPI	75	-	-	-	helicase-like protein
L_HIN0471	629	T3MO_BPPI	146	-	MTF2_METTP	78	adenine-specific type III m
S_HIN0472	194	-	-	-	-	-	-
L_HIN0473	197	RMH2_ECOLI	388	S46901	161	SC23CDS_13	67
M_HIN0474	399	LPXB_ECOLI	1141	SPSB_BACSU	54	-	ribonuclease HII
M_HIN0475	262	LPXA_YEREN	937	YVAT_BACSU	87	ATU22964_1	94
M_HIN0476	148	PMBZ_RICRI	314	YCSB_BACSU	84	-	lipid A disaccharide synthet
S_HIN0477	70	HU32781_8	opt101	-	-	-	acyl-[acyl-carrier-protein]
S_HIN0478	485	YUGX_ECOLI	111	-	-	-	(3R)-hydroxymyristoyl acyl
F_HIN0479	237	S45236	947	S51096	100	AKH_DAUCA	-
C_HIN0480	321	NRFQ_ECOLI	634	-	-	-	uridine 5'-monophosphate kin
C_HIN0481	nrfC	-	-	-	-	-	formate-dependent nitrite r
C_HIN0482	ntfB	ECOU089_118	226	MAPH_BACSU	155	FER_METBA	86
C_HIN0483	ntfA	NRFA_ECOLI	538	-	-	-	cytochrome precursor
L_HIN0484	1280	HRPA_ECOLI	935	-	-	-	cytochrome C552 precursor
R_HIN0485	Ygnd	YGND_ECOLI	2092	BSGENE_38	69	YMS2_CAEBL	418
R_HIN0486	150	GLPT_BACSU	156	YMDK_BACSU	112	-	helicase
C_HIN0487	378	APPB_ECOLI	67	GLPT_BACSU	67	-	membrane protein, new BCR
C_HIN0488	321	CYDA_ECOLI	1051	-	-	-	membrane protein
F_HIN0489	545	ECU29580_5	1257	-	-	-	cytochrome d complex termin
H_HIN0490	178	PNUC_ECOLI	2348	PYRG_BACSU	587	GLU30328_1	455
E_HIN0491	gltL	PNUC_ECOLI	98	-	-	-	cytochrome oxidase d subuni
E_HIN0492	257	YCKI_BACSU	611	YCKI_BACSU	611	S51433	CYP synthetase
N_HIN0493	238	YCKJ_BACSU	452	YCKJ_BACSU	452	-	integral membrane proteib
M_HIN0494	mutZ	YCKK_BACSU	362	YCKK_BACSU	362	S33754	glutamate/aspartate transp.
M_HIN0495	424	MUR2_EWTC	1369	MUR2_BACSU	643	AROA_BRANA	glutamine permease
L_HIN0496	85	ECOU067_118	212	-	-	-	glutamine-binding periplasm
L_HIN0497	105	ECOU067_119	60	RSBV_BACSU	59	-	UDP-N-acetylglucosamine eno
R_HIN0498	214	ECOU067_120	442	-	-	-	transcription regulator
R_HIN0499	167	ECOU067_121	375	-	-	-	minor sigma-37 factor
R_HIN0500	yrbF	ECOU067_122	998	-	-	-	-
R_HIN0501	yrbF	ECOU067_123	906	MKL_MYCIB	500	MDR1_MOUSE	membrane protein
C_HIN0502	soda	DSECN	342	SA4220SOD_1	218	S36129	transport ATPase
C_HIN0503	yejW	YEJW_ECOLI	777	PLNTRABC_4	137	ABCI_MOUSE	superoxide dismutase
C_HIN0504	yejV	YEJV_ECOLI	737	-	-	-	cytochrome c biogenesis tra
R_HIN0505	yejU	YEJU_ECOLI	709	U00018_1	84	-	cytochrome c biogenesis pro
R_HIN0506	yejM	YEJM_ECOLI	154	-	-	-	cytochrome c biogenesis pro
C_HIN0507	yejS	YEJS_ECOLI	304	-	-	-	inner membrane protein
C_HIN0508	yejR	YEJR_ECOLI	1668	U00018_1	105	-	cytochrome c biogenesis pro
O_HIN0509	yejQ	YEJQ_ECOLI	452	THI1_COHNB	82	YCK3_YEAST	cytochrome c biogenesis pro
HIN0510	yejP	YEJP_ECOLI	414	LUKS_STAU	68	SSN6_YEAST	thioredoxin-like cytochrome
HIN0511	44	-	-	-	-	-	thioredoxin-like, TPR repeat
HIN0512	102	-	-	-	-	-	-
	679	ECOLIG_1	1651	RMU10483_1	692	MMU15037_1	DNA ligase

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[illegible]



5	HIN609	CYSB	323	CYSB_ECOLI	885	M28509.1	196	-	Cys regulon transcriptional
1	HIN610	YfEB	314	YfCB_ECOLI	463	BSDNA320D.2	144	S51868	N6-adenine-specific DNA metJ
2	HIN611	-	167	-	-	-	-	-	phosphotransacetylase
3	HIN612	pta	711	ECOPTA_1	2125	PTA_BACU	575	PTA_METYE	acetate kinase
4	HIN613	ackA	401	ACKA_ECOLI	894	ACKA_BACU	431	-	acetic acid - firmeshift
5	HIN614	-	147	ECACKA	110	-	-	-	colicin V production (prote)
6	HIN615	CPVA	163	CPVA_ECOLI	508	-	-	-	anddiphosphoribosyltransfer
7	HIN616	purF	505	PURF_XBAC	930	PUR1_BACU	337	PUR1_SCHPO	DMP-glucose dehydratase
8	HIN617	-	256	SITLA_VIECH	76	A61316	69	YKAT_YEAST	arginine repressor
9	HIN618	argR	151	ARGR_ECOLI	523	AHRC_BACU	122	-	malate dehydrogenase
10	HIN619	mdh	311	ECODM67.165	1003	IDH_THERAO	166	MDH_YEAST	lysyl-tRNA synthetase
11	HIN620	lysU	502	ECODM93.45	1252	STASERR.1	720	HUMORFK15	peptide chain release factor
12	HIN621	prfB	370	RF2_ECOLI	1520	RR2_BACU	759	YSG18003.2	thiol-disulfide isomerase
13	HIN622	dhcC	229	DBRC_ERPCH	568	-	-	-	single-stranded-DNA-specific
14	HIN623	recJ	375	RCJC_ECOLI	935	-	-	-	thiol-disulfide interchange
15	HIN624	-	235	LTU15278.1	77	-	-	-	nucleosidase
16	HIN625	pfs	229	PFS_ECOLI	649	-	-	S39502	transferrin receptor
17	HIN626	-	913	MMU1858.1	101	-	-	-	L-lactate permease
18	HIN627	gmk	532	LDPD_ECOLI	218	KCY_BACU	476	KAD_CYPGA	cytidylate kinase
19	HIN628	rpsA	231	KCY_ECOLI	678	-	-	-	30S ribosomal protein S1
20	HIN629	hmd	549	RS1_ECOLI	2035	DBH_CLOBA	178	DBH_CRIPI	DNA-binding protein
21	HIN630	-	94	IHPB_SEBMA	291	YMDA_BACU	62	S43882	membrane protein
22	HIN631	-	97	-	62	-	-	-	-
23	HIN632	ycm	356	HUMORF1.1	82	BSU02604.3	73	HUMORF1.1	DNA-binding Zn finger prote
24	HIN633	pyrF	230	DCOP_ECOLI	743	DCOP_BACU	212	DCOP_EMENT	oxotidine-5'-phosphate deca
25	HIN634	yciH	106	YCIH_ECOLI	411	SLU21192.1	79	YRP1_METVA	new ACR, suII family, role
26	HIN635	-	221	539317	106	DNA_STRCO	84	-	Arpase (chromosomal replica
27	HIN636	uraA	414	URAA_ECOLI	505	PYPF_BACU	399	ANUPC.1	uracil permease
28	HIN637	upp	208	UPP_ECOLI	908	UPP_STREL	585	PUR1_YEAST	uracil phosphoribosyl trans
29	HIN638	dhax	688	DP3X_ECOLI	1092	BSDNA2X.1	617	G6U12438.1	Arpase (DNA replication)
30	HIN639	apt	478	APT_ECOLI	613	S52767	372	TAU22442.1	adenine phosphoribosyltrans
31	HIN640	lpd	180	ECACEX.4	1400	DLDH_BACU	630	DLDH_HUMAN	dihydrolipeamide dehydrogen
32	HIN641	aceF	567	XACEDP	1071	S14426	390	HUM2K.1	dihydrolipeamide acetyltran
33	HIN642	aceE	886	DEBCPV	1209	S24053	69	TKT_HUMAN	pyruvate dehydrogenase
34	HIN643	ycocG	152	YCOG_ECOLI	506	YRPF_BACU	305	-	-
35	HIN644	-	155	-	-	-	-	-	-
36	HIN645	-	367	ECOGUSRAB.6	145	-	-	-	-
37	HIN646	dhak	635	IOECDK	2264	DNAK_CLOAB	1185	H57M_PEA	Dnak chaperone
38	HIN647	dnaj	394	DNMJ_ECOLI	984	DNMJ_MYCIE	498	SCU1_YEAST	DnaJ chaperone
39	HIN648	proA	417	PROA_SEBMA	1327	PROA_BACU	630	ATPSCBSGN.1	gamma-glutamyl phosphate re
40	HIN649	ylcG	220	ECOLH82.12	340	-	-	-	integral membrane protein
41	HIN650	-	366	YIFK_ECOLI	64	STAGAPROC.4	60	LMPL_EBYC	permease
42	HIN651	bcr	398	BCR_ECOLI	867	TCMA_STREA	164	SC23CDS.22	permease
43	HIN652	yejD	232	YEJD_ECOLI	699	YPUL_BACU	161	-	pseudou synthetase
44	HIN653	-	206	-	-	-	-	-	-
45	HIN654	-	756	MAOX_BACST	639	MAOX_BACST	639	MAOC_PLARF	phosphate acetyltransferase
46	HIN655	-	647	MOOB_ECOLI	67	-	-	HUMARSBX.1	phosphoglycerol transferase
47	HIN656	uvrB	679	UVRB_ECOLI	2576	A42385	1224	HCA5_YEAST	exonuclease helicase, subun

Gene	Accession	Length	Start	End	Strand	Protein	Function
S_HIN0657	U00001.1	322	107	107	+	DnaK connector domain (?)	
L_HIN0658	U00001.1	206	107	107	+	homolog of virulence-associ-	
L_HIN0659	U00001.1	101	107	107	+	homolog of virulence-associ-	
L_HIN0660	U00001.1	107	107	107	+	transcript ATPase	
R_HIN0661	U00001.1	556	107	107	+	transcript ATPase	
R_HIN0662	U00001.1	127	107	107	+	transcript ATPase	
R_HIN0663	U00001.1	353	107	107	+	transcript ATPase	
S_HIN0664	U00001.1	74	107	107	+	transcript ATPase	
S_HIN0665	U00001.1	154	107	107	+	transcript ATPase	
L_HIN0666	U00001.1	1146	107	107	+	transcript ATPase	
L_HIN0667	U00001.1	466	107	107	+	transcript ATPase	
L_HIN0668	U00001.1	296	107	107	+	transcript ATPase	
H_HIN0669	U00001.1	437	107	107	+	transcript ATPase	
H_HIN0670	U00001.1	244	107	107	+	transcript ATPase	
L_HIN0671	U00001.1	358	107	107	+	transcript ATPase	
L_HIN0672	U00001.1	880	107	107	+	transcript ATPase	
S_HIN0673	U00001.1	587	107	107	+	transcript ATPase	
S_HIN0674	U00001.1	128	107	107	+	transcript ATPase	
S_HIN0675	U00001.1	27	107	107	+	transcript ATPase	
S_HIN0676	U00001.1	59	107	107	+	transcript ATPase	
L_HIN0677	U00001.1	38	107	107	+	transcript ATPase	
L_HIN0678	U00001.1	245	107	107	+	transcript ATPase	
P_HIN0679	U00001.1	263	107	107	+	transcript ATPase	
R_HIN0680	U00001.1	268	107	107	+	transcript ATPase	
R_HIN0681	U00001.1	238	107	107	+	transcript ATPase	
P_HIN0682	U00001.1	286	107	107	+	transcript ATPase	
L_HIN0683	U00001.1	682	107	107	+	transcript ATPase	
L_HIN0684	U00001.1	386	107	107	+	transcript ATPase	
C_HIN0685	U00001.1	220	107	107	+	transcript ATPase	
G_HIN0686	U00001.1	228	107	107	+	transcript ATPase	
R_HIN0687	U00001.1	72	107	107	+	transcript ATPase	
S_HIN0688	U00001.1	141	107	107	+	transcript ATPase	
L_HIN0689	U00001.1	495	107	107	+	transcript ATPase	
L_HIN0690	U00001.1	829	107	107	+	transcript ATPase	
L_HIN0691	U00001.1	1055	107	107	+	transcript ATPase	
L_HIN0692	U00001.1	459	107	107	+	transcript ATPase	
R_HIN0693	U00001.1	581	107	107	+	transcript ATPase	
L_HIN0694	U00001.1	128	107	107	+	transcript ATPase	
F_HIN0695	U00001.1	312	107	107	+	transcript ATPase	
L_HIN0696	U00001.1	377	107	107	+	transcript ATPase	
L_HIN0697	U00001.1	279	107	107	+	transcript ATPase	
L_HIN0698	U00001.1	261	107	107	+	transcript ATPase	
S_HIN0699	U00001.1	126	107	107	+	transcript ATPase	
L_HIN0700	U00001.1	178	107	107	+	transcript ATPase	
L_HIN0701	U00001.1	140	107	107	+	transcript ATPase	
L_HIN0702	U00001.1	140	107	107	+	transcript ATPase	
L_HIN0703	U00001.1	231	107	107	+	transcript ATPase	
L_HIN0704	U00001.1	509	107	107	+	transcript ATPase	

transcription-repair coupling factor  
DNA gyrase, subunit A  
homoserine acetyltransferase  
acetyltransferase  
P1tr-related ATPase  
membrane protein  
folylpolyglutamate synthase  
acetyl-CoA carboxylase beta  
membrane protease  
transcription-repair coupling factor  
hemin permease  
ferric enterobactin transporter  
SAM-dependent methyltransferase  
metal-binding protein  
telurite resistance protein  
tetracycline--tRNA synthetase  
chromosome partitioning ATPase  
oxygen-insensitive NAD(P)H isocitronate cytidyllyltransferase  
IS element  
new BCR  
transcription factor  
translation initiation factor  
type I restriction enzyme, B  
type I restriction enzyme B  
type I restriction enzyme B  
ribosome-binding protein  
pseudovirion synthetase  
chitinase mutase  
Zn finger protein  
aminotransferase  
nuclease, partitioning  
membrane protein  
permease  
deoxyguanosinetriphosphate

R_HIN0705	647	ECOW93_302	385	547441	356	CELFA2A10_5	240	transport ATPase
R_HIN0706	229	YADF_ECOLI	667	CINT1_SYN7	94	CHAC_TOBAC	124	carbonic anhydrase
R_HIN0707	477	SYCENT	2031	MC28_1	442	63KD_BRUMA	234	aspartagine--tRNA synthetase
R_HIN0708	173	RISB_ECOLI	605	RISB_BACU	334	S50974	129	riboflavin synthase beta chain
R_HIN0709	144	NUSE_ECOLI	376	-	-	-	-	transcription termination factor
R_HIN0710	345	YXHA_ECOLI	106	YXHA_BACU	106	PUR2_SCHPO	68	hydrogenase expression factor
R_HIN0711	163	pppa	314	-	-	-	-	phosphatidylglycerophosphate
R_HIN0712	210	YIGJ_ECOLI	140	-	-	-	-	integral membrane protein
R_HIN0713	270	DAPE_ECOLI	958	DAPE_BREIA	130	-	-	denydropicolinate reductase
R_HIN0714	82	YAE_ECOLI	203	S04543	106	UA0099	89	ferredoxin
R_HIN0715	253	-	-	-	-	-	-	-
R_HIN0716	329	SYFA_ECOLI	1257	SYFA_THERM	337	SYFM_YEAST	155	phenylalanyl-tRNA synthetase
R_HIN0717	795	ECOHIMA_4	2711	SYFB_BACU	350	MM10118_1	67	phenylalanyl-tRNA synthetase
R_HIN0718	96	HFA_ECOLI	322	DBH_BACU	186	DBH_CRYPH	156	DNA-binding protein
R_HIN0719	161	NIPC_ECOLI	382	S05542	108	-	-	lipoprotein
R_HIN0720	105	YIDK_ECOLI	211	PPCK_CHLTI	67	NAMI_CANPA	94	permease (incomplete ?)
R_HIN0721	194	YIDJ_ECOLI	125	-	-	ARS_CHLRE	70	sulfatase (incomplete ?)
R_HIN0722	271	PCU13148_1	83	-	-	SC6543_6	70	new ACR
R_HIN0723	199	ECOHIMA_1	698	S05346	445	-	-	initiation factor 3
R_HIN0724	65	R5EC35	239	R5B335	151	-	-	50S ribosomal protein L35
R_HIN0725	117	RI20_ECOLI	552	RI20_BACU	378	-	-	50S ribosomal protein L20
R_HIN0726	1211	EXSB_ECOLI	299	ADDA_BACU	73	HBYDH	97	exodeoxyribonuclease V, heli
R_HIN0727	640	ECU29581_30	269	-	-	YE06_YEAST	80	exodeoxyribonuclease V, heli
R_HIN0728	148	-	-	-	-	-	-	-
R_HIN0729	601	ION_BACBR	88	ION_BACBR	88	IONM_HUMAN	85	Ion/Sms-related endopeptidase
R_HIN0730	177	PABA_ECOLI	743	-	-	-	-	3-hydroxydecanoyl-l-acyl-car
R_HIN0731	242	CELFA57B9_4	72	-	-	CELFA57B9_4	72	metal-binding enzyme ?
R_HIN0732	89	R3RE15	360	R515_BACU	241	R515_HALMA	57	ribosomal protein S15
R_HIN0733	479	PEPPA_ECOLI	425	PEP_BACU	162	Y006_CABELI	70	D-alanyl-D-alanine carboxy
R_HIN0734	158	GREA_ECOLI	653	MU15183_7	120	-	-	transcription elongation fac
R_HIN0735	110	YBYE_ECOLI	231	CCMW_SYN7	81	-	-	new BCR
R_HIN0736	209	FTSJ_ECOLI	870	-	-	YBR1_YEAST	203	cell division, SAM-dependen
R_HIN0737	634	U01376_1	2204	FTSH_BACU	1208	CAATPASE_1	1091	ATP-dependent Zn-dependent
R_HIN0738	381	FTSH_ECOLI	1504	SYGCLR_118	474	YMEI_YEAST	716	truncated ATPase, partial d
R_HIN0739	275	ECOW67_105	743	DHPS_CIOAB	294	SA47154	142	dihydroperoxide synthase
R_HIN0740	445	MSEA_ECOLI	1528	U00070_23	405	S0POM_1	95	phosphomannomutase
R_HIN0741	164	-	-	-	-	-	-	-
R_HIN0742	129	S16259	162	YTXH_BACU	84	S16259	162	membrane protein
R_HIN0743	441	ECU29581_8	470	-	-	-	-	outer membrane protein
R_HIN0744	203	-	-	-	-	-	-	-
R_HIN0745	238	ECU29581_24	298	U00013_6	232	NFS1_YEAST	125	aminotransferase
R_HIN0746	439	YUXK_ECOLI	389	SA47441	356	CELFA2A10_5	173	transport ATPase
R_HIN0747	379	POTD_ECOLI	786	-	-	-	-	spermidine/putrescine-bind
R_HIN0748	247	POTC_ECOLI	945	MLU15180_37	188	-	-	spermidine/putrescine perme
R_HIN0749	286	POTB_ECOLI	925	CYST_SYN33	132	-	-	spermidine/putrescine perme
R_HIN0750	381	POTA_ECOLI	1210	MLU15180_38	603	MDR2_MOUSE	144	spermidine/putrescine trans
R_HIN0751	412	PEPT_SALTY	1094	-	-	-	-	peptidase T
R_HIN0752	160	BACMRGA_2	210	BACMRGA_2	210	-	-	DNA-binding protein





R	HIN0801		140	MDL_ECOLI	58	S49597	44	-	-	ATP-utilizing enzyme
I	HIN0802	holC	144	HOLC_ECOLI	361			-	-	DNA polymerase III, chi sub
C	HIN0803	func	464	FWNH_RAT	1369	FWNH_BACU	1028	ARLY_YEAST	97	funcinase
S	HIN0804		202	-	-	-	-	-	-	
P	HIN0805	pyrD	274	DP3A_BACSU	85	DP3A_BACSU	85	-	-	5'-3' exonuclease
R	HIN0806		339	PYRD_SALTY	1008	U00017_41	321	PYRD_DROME	315	dihydroorotate dehydrogenase
S	HIN0807		68	-	-	-	-	-	-	Sc/SwVI protein (plasmid pI)
S	HIN0808		182	S18665	118	-	-	-	-	
S	HIN0809		366	-	-	-	-	-	-	
S	HIN0810		118	-	-	-	-	-	-	
S	HIN0811		447	RP4TRANOF_	319	-	-	-	-	trans protein (plasmid)
S	HIN0812		436	-	-	-	-	-	-	
S	HIN0813		139	-	-	-	-	-	-	
R	HIN0814		374	-	-	-	-	-	-	
R	HIN0815		171	LLHOF168A_1	63	-	-	-	-	terminase large subunit ?
R	HIN0816		173	YG15_BP22	171	-	-	-	-	terminase small subunit
R	HIN0817		93	PRD1X11	108	-	-	-	-	bacteriophage protein
R	HIN0818		91	-	-	-	-	-	-	bacteriophage protein
CH	HIN0819		200	CH11_ORYSA	72	-	-	CH11_ORYSA	72	chitinase
R	HIN0820		118	VY11_BP22	73	-	-	-	-	bacteriophage lysis protein
I	HIN0821		201	BKSTATP_13	202	-	-	Y002_NPVAC	90	bacteriophage antirepressor
I	HIN0822		99	TRC4_ECOLI	73	-	-	-	-	primase?
S	HIN0823		97	-	-	-	-	-	-	
S	HIN0824		191	HTU32821_7	101	-	-	-	-	
R	HIN0825		94	pdb 11CC	59	-	-	-	-	transcription regulator ?
C	HIN0826	fnr	304	G45252	125	INTR_STRAM	57	EUPTEC11X_2	63	site-specific recombinase
S	HIN0827		257	FNR_ECOLI	985	NTCA_ANASP	102	-	-	funarate and nitrate reduct.
S	HIN0828		340	CBU10529_4	69	YCRB_THERH	68	-	-	new BCR
R	HIN0829		278	-	-	-	-	-	-	
R	HIN0830	putN	212	NGOT1A	197	-	-	-	-	
R	HIN0831	putM	344	PUR5_ECOLI	586	PUR3_BACU	325	HUMPGETA_1	412	phosphoribosylglycinamide f.
R	HIN0832	pydG	252	YDFG_ECOLI	882	PUR5_BACU	512	VU030895_1	518	phosphoribosylformylglycinam
R	HIN0833	trpB	397	ECUC23494_2	1704	HEFM_ANASP	144	SC9959_8	225	dehydrogenase
R	HIN0834	trpA	268	TRPA_VIBEA	578	TRPA_BREIA	956	TRP1_MALZE	953	tryptophan synthase, beta cI
R	HIN0835	usg	317	USG_ECOLI	259	DHAS_BACU	75	TRP_NEUCR	267	tryptophan synthase alpha cI
R	HIN0836		158	YBAK_SALTY	503	EBSC_ENTPA	182	-	-	dehydrogenase
R	HIN0837	cspD	72	CSPD_ECOLI	247	ARGOSP_1	161	GRP2_NICSY	136	transcription regulator ?
S	HIN0838		53	-	-	-	-	-	-	cold shock-like RNA-binding
J	HIN0839		243	ECU29581_5	536	YPUL_BACU	70	S50972	103	pseudou synthetase
S	HIN0840		106	RCU29581_6	161	-	-	-	-	
R	HIN0841		509	WGU39722_3	110	-	-	-	-	NTP-utilizing enzyme (GuaA)
I	HIN0842	xseB	84	BE7S_ECOLI	222	-	-	-	-	exodeoxyribonuclease VII sm
H	HIN0843	1spA	295	1SPA_BACU	384	GAPP_CAPAN	361	geranylgeranyltransfer		transferase
I	HIN0844		625	YVUX_RHCA	592	MLU15181_22	460	HUMECKDH_1	104	guanylate kinase 1
R	HIN0845	sspB	150	SSPB_ECOLI	378	-	-	-	-	stringent starvation protei
O	HIN0846	sspA	212	RGECS5	661	-	-	-	-	stringent starvation protei
J	HIN0847	rpsI	130	ECUW67_159	566	RS9_BACST	330	R61A_YEAST	59	30S ribosomal protein S9
J	HIN0848	rplM	142	RL13_HABSO	710	RL13_STACA	429	RL13_YEAST	48	ribosomal protein L13

E	HIN0849	metF	292	METF_ECOLI	1132	-	HSU09806.1	220	5,10-methylentetrahydrofoli-
H	HIN0850	biOD	242	BIOD_ECOLI	275	-	COBQ_METVO	56	dechlorobiotin synthetase
H	HIN0851		107	-					
H	HIN0852	fclE	218	ECOHU47_44	654	SP16156_3	PC1117	289	GTP cyclohydrolase I
H	HIN0853	meoA	404	MOEA_ECOLI	868	STREXPI0A.1	GEPI_RAT	261	molybdoprotein biosynthesis ]
H	HIN0854	meoB	243	MOEB_ECOLI	788	S40167	YHR1_YEAST	302	molybdoprotein biosynthesis ]
I	HIN0855		107	ECOCIS	148				affects resistance to novob.
R	HIN0856		195	SPU1267_2	70				membrane protein
O	HIN0857		156	PLIB_NECO	108	RESA_BACSU	S34275	59	thioredoxin
O	HIN0858		213	BSYKTCDA_4	104	BSYKTCDA_4			chaperone ?, cytochrome b/c
O	HIN0859		353	EXP3_STPM	538	EXP3_STPM	YEN2_YEAST	234	peptide methionine sulfoxid
S	HIN0860		168	-					
R	HIN0861		178	NSU12287_1	68	-			opacity (membrane) protein
R	HIN0862		134	CPVANH_4	81	CPVANH_4	-		immunity repressor protein
L	HIN0863		194	RPSH_PSEAE	118	SIGX_BACSU	85		RNA polymerase sigma-E factor
M	HIN0864		176	YADA_YERPS	123	-			invasin
R	HIN0865		454	FUSA_BORCE	179	-			outer membrane protein
M	HIN0866		445	MESA_ECOLI	1528	U00020.23	SOPGM_1	95	phosphomannomutase
R	HIN0867		275	ECOU67_105	743	DHPS_CLDAB	S47154	142	diacylglycerol kinase
P	HIN0868	fhua	739	YEF0XAG_1	149				transcription factor
J	HIN0869		589	S47044	160				transcription factor
J	HIN0870		89	R3C015	360	RS15_BACST	241	160	transcription factor
P	HIN0871		115	MODA_ECOLI	90			57	transcription factor
H	HIN0872	fepC	253	MSU10425_3	209	MSU10425_3	MDR_PLAIF	130	transcription factor
R	HIN0873	fepD	337	FEUB_BACSU	276	FEUB_BACSU	VTM1_RAT	46	transcription factor
F	HIN0874		351	FEUA_BACSU	65	FEUA_BACSU	-		transcription factor
R	HIN0875		281	MODD_PEOCA	302	U00010.13	97		transcription factor
R	HIN0876		199	MBPX_MARPO	230	XYDL_BACSU	NADC_YEAST	95	transcription factor
R	HIN0877		113	NIFC_CLOPA	110	NIFC_CLOPA	MDR1_CAREL	118	transcription factor
R	HIN0878	sfsB	239	S13498	154				transcription factor
L	HIN0879		89	DBNE_BPD10	136				transcription factor
R	HIN0880		687	PMUATNP_1	104				transcription factor
R	HIN0881		90	TRA_BPMU					transcription factor
S	HIN0882		156	-					transcription factor
R	HIN0883		287	VPB_BPMU	411	ATMP_STRAU	72		transcription factor
S	HIN0884		105	-					transcription factor
R	HIN0885		169	PMULEFTEN_1	477				transcription factor
PWIR	HIN0886		113	PMULEFTEN_2	243				transcription factor
S	HIN0887		90	-					transcription factor
S	HIN0888		73	-					transcription factor
S	HIN0889		57	-					transcription factor
S	HIN0890		186	-					transcription factor
R	HIN0891		185	PMULEFTEN_3	104				transcription factor
R	HIN0892		184	-					transcription factor
R	HIN0893		146	VPC_BPMU	177				transcription factor
S	HIN0894		168	-					transcription factor
S	HIN0895		94	-					transcription factor
R	HIN0896		116	NAAA_BPT3	175				transcription factor

lysosome

[illegible]

H	HIN0945	yabF	202	DHOV_HUMAN	156	-	DHOV_HUMAN	156	NAD (P)+H:menadiione oxidoredu	
R	HIN0946	y9J1	414	YGJ1_ECOLI	1203	GLTT_BACST	101	BOVENSOGAT_	127	amino acid permease
L	HIN0947	unmd	140	SAMA_SALTY	140	-	-	-	SOS mutagenesis protein, au	
R	HIN0948	arog	362	AROG_ECOLI	926	AROF_CORGL	496	AROG_YEAST	736	phospho-2-dehydro-3-deoxyhep
M	HIN0949	-	416	ZMDNAGR_3	250	-	-	-	membrane protein (FtsX para	
R	HIN0950	-	227	BAU11045_1	547	YXDU_BACSU	425	MDR1_PAT	183	transport ATPase
H	HIN0951	-	191	SMABIO_5	191	BRBLIOAD_2	133	COQ3_METVO	58	dehydrobiotin synthetase (Bti
H	HIN0952	bioC	260	BIOC_ECOLI	57	YAT1_SYND6	56	COQ3_YEAST	54	SAM-dependent methyltransfer
S	HIN0953	-	215	-	-	-	-	-	-	-
H	HIN0954	bioF	380	XUECCA	218	BIOF_BACSH	175	HEM0_OPST4	167	8-amino-7-oxononanoate synt
R	HIN0955	bioA	430	XNECDP	1155	U00010_25	600	OAT_PLAFA	199	adenosylmethionine--8-amino
R	HIN0956	-	393	ZMDNAGR_3	174	AMIC_STRFN	77	-	permease	-
R	HIN0957	-	315	SERA_BACSU	234	SERA_BACSU	234	PDH_NEUCR	206	dehydrogenase
S	HIN0958	-	118	-	-	-	-	-	-	-
M	HIN0959	kdsA	284	ECU18555_9	1223	AROG_BACSU	122	-	-	oxy-D-manno-octulosonic aci
S	HIN0960	ycha	267	ECU18555_8	218	-	-	-	-	adenyine-specific DNA methyl
H	HIN0961	hemK	292	ECU18555_6	325	BSDNA320D_2	106	COQ3_YEAST	53	peptide chain release facto
S	HIN0962	-	156	-	-	-	-	-	-	-
U	HIN0963	prfA	361	ECU18555_5	1432	MLU15186_18	496	YSC18003_2	119	site-specific recombinase
S	HIN0964	-	52	-	-	-	-	-	-	pyruvate kinase type II
R	HIN0965	-	178	-	-	-	-	-	-	replicative helicase
R	HIN0966	-	990	TB12_NEIME	219	P60_LISIN	69	S14548	99	alanine racemase
R	HIN0967	-	138	VFG_BPMU	82	-	-	-	-	glucose-6-phosphatase
S	HIN0968	-	169	-	-	-	-	-	-	glycocylyltransferase
R	HIN0969	-	366	G45252	149	-	-	-	-	colicin
C	HIN0970	pykA	478	S29790	1846	S27330	384	S41379	475	site-specific recombinase
L	HIN0971	dnab	504	DNAB_SALTY	726	DNAC_BACSU	400	-	-	pyruvate kinase type II
G	HIN0972	alt	360	ALR1_SALTY	485	ALR_BACST	194	-	-	replicative helicase
R	HIN0973	pgi	563	ECOUW88_72	1524	CHTITUA_1	195	G6PI_PIG	747	alanine racemase
R	HIN0974	yibD	323	NGU14554_5	226	SFSA_BACSU	111	ALG5_YEAST	57	glucose-6-phosphatase
N	HIN0975	-	155	PCR_YEREN	204	-	-	-	-	glycocylyltransferase
S	HIN0976	-	139	-	-	-	-	-	-	colicin
J	HIN0977	args	577	SYR_ECOLI	2184	SYR_BRBLA	127	SYR_CRILIO	333	arginyl-tRNA synthetase
E	HIN0978	llvH	163	S15940	567	CORBA1_3	277	YCA9_YEAST	187	acetylactate synthase III s
R	HIN0979	llvI	573	LLV1_ECOLI	1295	A44857	797	ILV6_PORUM	736	acetylactate synthase III s
R	HIN0980	-	519	HTU32790_7	88	YWFA_BACSU	51	-	-	permease
L	HIN0981	stpa	134	STPA_ECOLI	306	-	-	RL22_HALHA	55	DNA-binding protein
F	HIN0982	putu	278	PURU_ECOLI	1059	CSU23955_6	477	PUR2_HUMAN	198	formyltetrahydrofolate hydr
E	HIN0983	arocA	432	PHU03068_1	1445	AROA_BACSU	117	ARQA_ARATH	251	5-enolpyruvylshikimate-3-ph
L	HIN0984	ycau	446	YSS2_COXBU	1006	BSDNAZX_1	73	YNO2_YEAST	258	ATPase (DNA replication)
S	HIN0985	-	205	YSS1_COXBU	177	-	-	-	-	-
R	HIN0986	-	529	SF3E_COXBU	699	SF3E_BACSU	602	BHS_MOUSE	66	ATPase
S	HIN0987	-	223	-	-	-	-	-	-	-
S	HIN0988	-	107	SP3E_COXBU	87	-	-	-	-	-
R	HIN0989	ltp	166	LTP_SALTY	624	-	-	-	-	leucine responsive regulato
O	HIN0990	sms	475	SMS_ECOLI	1699	YACU_BACSU	853	LONM_HUMAN	99	ATPase, ATP-dependent prote
S	HIN0991	ygiP	352	YGIF_ECOLI	187	-	-	-	-	-
S	HIN0992	-	238	-	-	-	-	-	-	-

S	HIN0993	317	-	-	-	-	-	phosphate permease	
S	HIN0994	95	-	-	-	-	-	myosin-like (coiled coil) p	
S	HIN0995	151	YQJF_ECOLI	-	-	-	-	tRNA nucleotidyltransferase	
S	HIN0996	226	-	-	-	-	-	5-aminolevullinate synthase	
P	HIN0997	420	RATRAM1A_1	428	MIUJ5167_34	169	RATRAM1A_1	428	phosphatase
R	HIN0998	203	YGIN_ECOLI	272	-	152	A46514	93	ADP-ribose transferase
J	HIN0999	416	COA_ECOLI	893	PAPS_BACSU	152	TNT_YEAST	66	ADP-ribose transferase
H	HIN1000	209	HEMW_SALTY	239	-	-	-	-	ADP-ribose transferase
R	HIN1001	321	YCHB_ECOLI	663	YASH_BACSU	297	OAT_VIGAC	49	ADP-ribose transferase
F	HIN1002	315	KIEBT_ECOLI	710	UN0886	367	S51270	583	tyrosyl-tRNA synthetase
J	HIN1003	401	SYX_THIIE	882	S16426	773	YSCMSY1A_1	150	sugar fermentation stimulat
G	HIN1004	238	SPSA_ECOLI	623	-	-	-	-	permease
K	HIN1005	464	YDHE_ECOLI	307	-	-	YH2_YEAST	145	riboflavin alpha subunit
E	HIN1006	204	RISA_ECOLI	695	RISA_BACSU	182	SCC10RF_4	228	aminopeptidase N
H	HIN1007	869	AMPN_ECOLI	2072	S38364	144	AMPB_MOUSE	165	phosphoribosylaminoimidazo
F	HIN1008	164	DECEK	621	PUR6_BACSU	504	PUR6_SCHPO	369	phosphoribosylaminoimidazo
F	HIN1009	362	DECEK	428	PURK_BACSU	185	PUR6_SCHPO	197	aspartate aminotransferase
C	HIN1010	396	pdh11AAW	1329	-	-	S46316	562	hydrogenase (disrupted)
C	HIN1011	45	HYBE_ECOLI	146	-	-	-	-	transport ATPase
R	HIN1012	205	PFU13043_1	192	PFU13043_1	192	GC20_YEAST	128	-
S	HIN1013	95	-	-	-	-	-	-	-
S	HIN1014	167	-	-	-	-	-	-	-
S	HIN1015	206	-	-	-	-	-	-	-
S	HIN1016	161	-	-	-	-	-	-	-
R	HIN1017	227	-	-	-	-	-	-	-
K	HIN1018	177	A32239	189	MERR_BACSR	185	-	-	transcription regulator
K	HIN1019	165	S50869	101	-	-	-	-	permease
R	HIN1020	238	POTE_ECOLI	46	GLPT_BACSU	68	YIF1_YEAST	84	dehydrogenase? new ACR
R	HIN1021	116	YABJ_BACSU	92	YABJ_BACSU	92	-	-	alkaline phosphatase-like, )
R	HIN1022	134	ECOM67_162	165	-	-	-	-	50S ribosomal protein L25
R	HIN1023	212	DRDA_ECOLI	100	UN0011_31	91	-	-	-
J	HIN1024	95	RL25_ECOLI	309	CTIC_BACCL	71	-	-	-
S	HIN1025	190	-	-	-	-	-	-	-
E	HIN1026	121	KIECD3	181	AKAB_CORGL	56	MZEAKHD_1	64	aspartate kinase
F	HIN1027	432	ECOM93_89	1769	BAC160K_2	643	PURA_DICDI	640	adenylosuccinate synthetase
F	HIN1028	303	DAED_ACTPL	1356	ES3402	78	AT030298_1	81	tetrahydrodipicolinate N-su
F	HIN1029	349	PURR_ECOLI	481	CLOREPA_1	267	-	-	purine synthesis repressor
C	HIN1030	879	CAP_ECOLI	1973	UN0013_25	309	CAP2_SORVU	1095	phosphoenolpyruvate carboxy
R	HIN1031	470	GBQ_LYNST	45	-	-	GBQ_LYNST	45	-
E	HIN1032	565	SAPA_SALTY	369	DPPE_BACSU	125	-	-	peptide transport periplasm
E	HIN1033	321	SABP_SALTY	556	DPBP_BACSU	159	YFRO_YEAST	63	oligopeptide permease
E	HIN1034	295	SAPC_SALTY	658	APPC_BACSU	200	TAP1_HUMAN	95	dipeptide permease
E	HIN1035	349	SAPD_SALTY	1155	APPD_BACSU	292	-	-	transport ATPase
E	HIN1036	266	SAPF_SALTY	673	APPF_BACSU	326	CEDH11_3P	119	peptide transport ATPase
F	HIN1037	338	YEHF_ECOLI	876	-	-	-	-	integral membrane protein
F	HIN1038	269	TRPA_ECOLI	975	-	-	-	-	pseudon synthetase I
C	HIN1039	333	FlpP_ECOLI	918	NOSFTZODP_1	284	CBE02H1_2	70	fructose-1,6-bisphosphatase
C	HIN1040	222	KEY_ECOLI	605	KCY_BACSU	453	FlpP_WHEAT	310	fructose-1,6-bisphosphatase
C	HIN1049	222	KEY_ECOLI	605	KCY_BACSU	453	KAD_CYPA	86	cytidylate kinase

E HINI1041	291	YAAD_BACSU	931	SC6543_3	630	indole-3-glycerol-phosphate
E HINI1042	175	YAAE_BACSU	235	YFG0_YEAST	68	aminotransferase
I HINI1043	564	DERCDL	1266	DMG0506_1	63	D-lactate dehydrogenase
S HINI1044	36	TIR1_ECOLI	99	-	-	Fragment of hsdR protein (?)
R HINI1045	92	HU32707	243	-	-	11pOprotein
R HINI1046	183	MLPC_ECOLI	179	S05542	115	Zn protease
R HINI1047	484	ECOW67_173	821	S44956	79	methyltransferase? new ACR
R HINI1048	283	ECOW67_76	850	YABC_BACSU	458	-
S HINI1049	575	ECOW67_77	252	-	-	-
S HINI1050	119	ECOW67_78	251	-	-	-
R HINI1051	194	ECOW67_79	367	-	-	-
H HINI1052	193	ECOW67_80	481	YGS2_ANACE	65	phosphoheptose isomerase
R HINI1053	781	RIR1_ECOLI	3299	MSGROR_1	170	hemolysin precursor? new BCI
F HINI1054	376	RDCZR	1687	-	-	ribonucleoside-diphosphate
C HINI1055	409	ODO2_ECOLI	1071	ODO2_BACSU	535	2-oxoglutarate dehydrogenas
C HINI1056	950	ODO1_ECOLI	2580	ODO1_BACSU	532	metal-utilizing enzyme (?)
R HINI1057	212	U00011_3	156	YABD_BACSU	45	new BCR
S HINI1058	259	YJUV_ECOLI	59	-	-	-
S HINI1059	127	-	-	-	-	-
S HINI1060	489	HSAS8B011	134	-	-	-
C HINI1061	695	A41798	622	YPER_SYMP2	114	carboxy-terminal membrane p:
S HINI1062	41	YebJ	90	-	-	-
R HINI1063	157	-	-	-	-	-
R HINI1064	416	PQIA_ECOLI	238	-	-	paraquat-inducible protein
H HINI1065	881	PQIB_ECOLI	145	-	-	paraquat-inducible protein?
H HINI1066	150	S31883	472	-	-	polyporexin converting f:
H HINI1067	81	MOAD_ECOLI	267	-	-	polyporexin
H HINI1068	160	S31881	378	-	-	polyporexin converting f:
H HINI1069	337	MOA_ECOLI	941	ANNOA_1	272	polyporexin cofactor biosynt
S HINI1070	223	YTFE_ECOLI	521	-	-	polyporexin cofactor biosynt
F HINI1071	337	KSP1_ECOLI	666	GLMS_BACSU	109	hexose phosphate aminotrans:
S HINI1072	180	ECOW67_126	206	-	-	-
S HINI1073	718	ECOW67_282	241	-	-	-
S HINI1074	221	YOM2_PHOS9	96	-	-	-
R HINI1075	353	SOHB_ECOLI	797	-	-	periplasmic protease
C HINI1076	192	S33895	564	RESC_BACSU	59	membrane protein
C HINI1077	193	S33894	193	S49997	81	ferredoxin
C HINI1078	819	S33893	268	M24_STREPY	110	membrane protein, NADH:ubiq
C HINI1079	358	S33892	292	-	-	membrane protein, NADH:ubiq
C HINI1080	235	S33906	284	-	-	membrane protein, NADH:ubiq
C HINI1081	207	S33906	492	-	-	membrane protein, NADH:ubiq
R HINI1082	211	IABK	930	END3_BACSU	340	membrane protein, NADH:ubiq
R HINI1083	457	S56968_1	195	-	-	membrane protein, NADH:ubiq
P HINI1084	351	MOOC_ECOLI	759	MSMK_STPMU	232	membrane protein, NADH:ubiq
P HINI1085	229	MOB_ECOLI	781	CYSW_STMP7	205	membrane protein, NADH:ubiq
P HINI1086	254	MODA_ECOLI	417	BACORA_4	69	membrane protein, NADH:ubiq
P HINI1087	255	MODA_ECOLI	203	-	-	membrane protein, NADH:ubiq
E HINI1088	267	EXAMASL_8	487	YWDF_BACSU	74	glycosyl transferase

R_HIN1089	294	YMDF_BACSU	109	YMDF_BACSU	109	BOVUDP_1	67	glycosyl transferase
M_HIN1090	257	HU05670_2	66					lipopolysaccharide synthase
M_HIN1091	353	rfAB	297	YAGE_BACSU	187	PIGA_HUMAN	79	UDP-D-galactose: (glucosyl) 1-
S_HIN1092	304							lipopolysaccharide biosynth
M_HIN1093	247	S30030	88			PEM1_YEAST	46	
M_HIN1094	247	YCBC_ECOLI	58					5-methyltetrahydrofolate--h
E_HIN1095	756	A42863	1261			CRMETS_1	931	permease
E_HIN1096	372	YJGP_ECOLI	570					permease
E_HIN1097	372	YJGP_ECOLI	934					leucyl aminopeptidase
E_HIN1098	491	AMPA_ECOLI	1035			AMP1_ARATH	359	histidine kinase, sensor
B_HIN1099	669	BEFTT_ECOLI	318	MYCAMINO_1	253			transcription regulator, re
R_HIN1100	451	ECU28377_12	787	YACL_BACSU	59			two-component system frame:
R_HIN1101	YGLX	ECU28377_12	689	U00018_36	101			
R_HIN1102	YGLW	ECU28377_12	161	RCAC_FREDI	339	SKN7_YEAST	139	
G_HIN1103	46	APCTI	79					
G_HIN1104	166	WOCOP3	584	S46952	357	S74697_1	260	phosphotransferase system e
G_HIN1105	575	PT1_SALTY	2087	PT1_BACST	1359	PTPDKQ_2	116	phosphoenolpyruvate--protein
G_HIN1106	85	pdb110H	326	S37585	154			phosphotransferase phosphoc
R_HIN1107	YJGO	YJGO_ECOLI	427	ATPB_BACST	86	CEL34E10_1	82	Grpase
S_HIN1108	182	YJBR_ECOLI	715					
M_HIN1109	355	S30678	524	MRAY_BACSU	131	GPT_MOUSE	63	undecaprenyl-phosphate alphi
S_HIN1110	261							
E_HIN1111	863	S36254	831					PIT uridylyl-transferase
R_HIN1112	188	NGOPUSAA_4	173	LJU09558_1	115			IS-150 insertion element pr
R_HIN1113	216	A33595	395	A33595	395			IS-150 insertion element pr
J_HIN1114	268	S12027	499	AMPM_BACSU	347	YSCU9672_5	389	methionine aminopeptidase
R_HIN1115	114	YADR_ECOLI	504	S49955	184	SC9499X_22	105	new ACR, nitrogen fixation
S_HIN1116	117	yeaB	120					
S_HIN1117	781	S45218	709	PBPB_BACSU	252			penicillin-binding protein,
E_HIN1118	306	JC2039	452	PUD7_STRPN	67	JC2039	452	SATCAR synthetase
E_HIN1119	444	ECOUW67_101	1665	JUN0505	1559	ASSY_BOVIN	149	axialinosuccinate synthase
E_HIN1120	397	YC5H_BACSU	495	MLU15184_8	59			branched-chain amino acid c
R_HIN1121	245	YC5F_BACSU	314			LAMB_EMENT	246	lactam utilization protein
R_HIN1122	522	YSCUAMD_1	191	YCSJ_BACSU	133	YSCUAMD_1	190	(urea ?) amidolyase
M_HIN1123	1020	HU32846_1	171					adhesin
M_HIN1124	298	AIDA_ECOLI	88					adhesin
L_HIN1125	659	RNB_ECOLI	529	YH11_LACIA	75	D183_SCHPO	97	exonuclease II
J_HIN1126	295	FABI_ECOLI	978	YNT3_ABRN	411	FABI_BRANA	160	enoyl-l-acyl-carrier-protein
J_HIN1127	527	RF3_ECOLI	2387	EPG_SPIPL	233	S44896	151	peptide chain release facto
S_HIN1128	77							
S_HIN1129	109							
E_HIN1130	244							
E_HIN1131	309	METR_ECOLI	326	ALSR_BACSU	160	S43767	67	transcriptional activator o
E_HIN1132	381	L1DD_ECOLI	1534	AB012219_1	265	S33322	323	l-lactate dehydrogenase (cy
E_HIN1133	269	ECOUW89_26	505	IBAGR_1	165			glutamate racemase
E_HIN1134	693	REGG_ECOLI	2376	MPD_BACSU	313	S30805	93	DNA recombinase, helicase
F_HIN1135	677	SPOT_ECOLI	1254	S39975	764			pppGp 3' pyrophosphohydroly
L_HIN1136	88	RPOZ_ECOLI	279					DNA-directed RNA polymerase



F	HINI137	gmk	208	KGA_ECOLI	434	MEH02537.2	57	KIBYU	177	guanylate kinase
E	HINI138	gapa	143	G3P_ESCSE	302	S603GAP1.1	248	GBILYADEN	298	glyceraldehyde-3-phosphate
I	HINI139		607	SC9408_8	204	BS026444.3	136	SC9408_8	204	long-chain-fatty-acid CoA l
R	HINI140	yida	262	YIDA_ECOLI	198	YPDA_BACST	159	ATCB_DROME	77	hydroxylase
C	HINI142	fdhd	154	U00016_19	130	U00016_19	130			metal-binding protein (?)
C	HINI143	fdhd	270	FDHD_ECOLI	515	NARO_BACSU	123			formate dehydrogenase forma
C	HINI144	fdmh	1028	FDMG_ECOLI	1742	NACB_BACSU	164	FDHA_METRO	228	formate dehydrogenase, nitro
C	HINI145	fdmh	312	FDMH_ECOLI	972	NAMH_BACSU	161	FBR_METSA	76	formate dehydrogenase, nitro
C	HINI146	fdmh	203	FDNI_ECOLI	460					formate dehydrogenase, nitro
C	HINI147	fdmh	302	FDHE_ECOLI	678					formate dehydrogenase, nitro
J	HINI148	riat	155	RIAT_ECOLI	327					formate dehydrogenase, nitro
L	HINI149	hold	134	HOLD_ECOLI	112	STRA_STRIA	73	YFB7_YEAST	60	ribosomal-protein-alanine ar
R	HINI149	yj1t	330	YJUT_ECOLI	495	SARP_LARO_2	91	HSHIOWT9_3	74	DNA polymerase III, psi sub
R	HINI150	erc	302	ERA_ECOLI	1203	BRX_BACSU	387	WSSL_YEAST	120	SAM-dependent methyltransfer
L	HINI151	erc	227	RNC_ECOLI	661	MG35_1	105	PACI_STEAT	155	GTP-binding protein
M	HINI152	lepb	349	LEPB_ECOLI	439	LEPC_BACST	87	YME1_YEAST	74	ribonuclease III
M	HINI153	lepb	598	LEPB_ECOLI	1524	U00016_9	1381		492	signal peptidase I
L	HINI154	yfid	127	YFID_ECOLI	543					membrane gtpase
R	HINI155	ung	219	DGBEU	827	UNG_BACSU	380	UMG1_HUMAN	615	putative mobile protein hom
R	HINI156		474	S49379	1521	U00019_14	384	CELF2B5_2	249	uracil-DNA glycosylase
R	HINI157	yj1e	476	ECU28379_10	301	S0013238_1	205			oxidoreductase (sulfur-iron
R	HINI158		419	KPCITCDHF_5	265					2-oxoglutarate/malate trans
I	HINI159		500	KPCITCDHF_4	1546					citrate metabolism operon li
S	HINI160		291	CILB_KLEBN	540					citrate lyase alpha-subunit
S	HINI161		95	KPCITCDHF_2	178					citrate lyase beta-subunit
I	HINI162		335	KPCITCDHF_1	686					acetate:SH-citrate lyase li
H	HINI163	lipa	320	LIPA_ECOLI	1184	S19702	62	LIP5_YEAST	373	lipid acid synthase
H	HINI164	lipb	212	LIPB_ECOLI	211			S51458	125	lipote protein ligase B
M	HINI165	ybeb	92	YBBB_ECOLI	352					
M	HINI166	daca	393	DACA_ECOLI	467	DACF_BACSU	208			D-alanyl-D-alanine carboxyp
M	HINI167	clpa	287	CLPA_ECOLI	202					rare lipoprotein A
M	HINI168	mrdb	371	RODA_ECOLI	1212	SPSE_BACSU	231			rod shape determining prote
M	HINI169	mrda	651	PBP2_ECOLI	1852	A36903	215			penicillin-binding protein,
S	HINI170	ybea	155	YBEA_ECOLI	703					
S	HINI171	ybeb	102	YBBB_ECOLI	231					
G	HINI172	yidr	551	YBBB2_E50	1283					Yme2_CAEEL
R	HINI173		592	YDDA_ECOLI	167	COMA_STERN	110	CEIC44B7_7	132	new ACR
O	HINI174	mrdb	378	ECOMW6_181	959	MRBB_BACSU	381	PCGRPA_1	119	PTS system IIC component
M	HINI175	mrcc	351	MRBC_ECOLI	771	BACITVBE6_4	99			transport ATPase
M	HINI176	mrdb	162	MRBD_ECOLI	361	MRBD_BACSU	86			rod shape determining prote
S	HINI177	xtha	258	YUGD_ECOLI	63					rod shape determining prote
J	HINI178		267	EX3_ECOLI	1050	EXOA_BACSU	134	DDU31631_1	95	exodeoxyribonuclease III
L	HINI179		224	YF11_ECOLI	121	MGU02214_1	76	SPAC18B11_2	99	penicillin synthetase
S	HINI180	ycjF	354	YCF1_YCF1	139					
S	HINI181	ycdA	220	YCQA_ECOLI	696	ARSB_STAAU	51	DRONDA_1	82	penemase
R	HINI182	ycdA	184	YTFJ_ECOLI	374					transcription regulator
C	HINI183	phnA	120	PHNA_ECOLI	223	PHNA_STRNAU	130			aldehydophosphate uptake pro
C	HINI184	eda	212	ALNH_EBROW	415					4-hydroxy-2-oxoglutarate al

C	HIN1185	hdbA	285	NOSH8MA_1	156	NOSH8MA_1	156	A48674	116	7-alpha-hydroxysteroid dehy
G	HIN1186	yJhI	314	C55215	506	RBSK_BACSU	85	SCRK_SOLUT	87	2-dehydro-3-deoxygluconokin
R	HIN1187		427	YJAN_ECOLI	617					permease
R	HIN1188		165	YJAM_ECOLI	152	JN0768	69	DDRNPART_1	70	integral membrane protein
C	HIN1189		328	DCTP_RHOCA	238					periplasmic binding protein
C	HIN1190		342	RSPB_ECOLI	263	A45052	145	DH80_SCHPO	154	dehydrogenase
G	HIN1191	uxuR	266	UXUR_ECOLI	304	S33420	116			uxu operon regulator
G	HIN1192	uxuA	394	UXUA_ECOLI	1579					mannonate hydrolase
R	HIN1193	yxdO	237	KRPCK2_2	384					membrane protein
L	HIN1194	yvrc	609	UVRC_ECOLI	1168	UVRC_BACSU	283	ERCI_MOUSE	85	exonuclease
M	HIN1195	kdsB	254	A26322	595	CTU15192_1	159	YSC1AF60A_1	79	3-deoxy-nanno-octulosonate
R	HIN1196	ycaB	332	YCAH_ECOLI	380	SPU16156_2	69			ATP-utilizing enzyme
R	HIN1197	msbA	587	MSBA_ECOLI	1065	SAU29478_1	582	PMD1_SCHPO	523	transport ATPase
O	HIN1198	ycaI	788	CME3_BACSU	152	CME3_BACSU	152			integral membr. protein new
O	HIN1199	dksA	145	DKSA_ECOLI	575	Y2MB_BACSU	106			dosage-dependent dnaK suppl
L	HIN1200	penB	452	PCNB_ECOLI	1015	PAP5_BACSU	161	TNT_YEAST	82	poly(A) polymerase
H	HIN1201	foIk	160	HPFK_BACSU	283	HPFK_BACSU	283	FAS_PNECA	248	2'-smino-4-hydroxy-6-hydroxy
R	HIN1202	yJee	158	YJEE_ECOLI	415	U00020_7	83	YPT7_YEAST	41	ATP-utilizing enzyme
M	HIN1203	ambB	432	AMIB_ECOLI	347	CMBB_BACSU	98			N-acetylmutamoyl-L-alanine
J	HIN1204	mutL	629	MUTL_SALTY	964	HEMB_STRPN	328	HSHML1_1	453	DNA mismatch repair protei
L	HIN1205	miaA	311	MTAA_ECOLI	1094	U00019_10	177	MOD5_YEAST	255	TRNA delta(2)-isopentenylp
E	HIN1206	glnR	981	GLNR_ECOLI	724	RECN_BACSU	297	A46475	249	glutamate-ammoma-L-ligase ad
R	HIN1207	tecN	558	RECN_ECOLI	970		199	YEP1_YEAST	212	DNA repair protein, ATPase
O	HIN1208	yJfB	285	YFJB_ECOLI	305	U00021_19	177	GRPE_YEAST	130	ATP-utilizing enzyme, kinase
O	HIN1209	grpE	234	GRPE_ECOLI	192	S08418	58			heat shock protein
R	HIN1210		114	S51882	64	A61153				adenyl/yltransferase
F	HIN1211	nrtd	146							anaerobic ribonucleotide re
R	HIN1212	tesB	286	ECOTESB_1	789			YMEB_YEAST	133	thioesterase
S	HIN1213		288							
J	HIN1215	cyss	459	SYC_ECOLI	1707	SYC_BACSU	567	HMCYSTRNA_1	273	cyteinyI-tRNA synthetase
S	HIN1217	ppib	169	CYPB_ECOLI	450	CYPB_SAMP7	120	CER59E10_1	153	peptidyl-prolyl cis-trans i
S	HIN1218		143	S73874	169					
S	HIN1219	yJjV	262	XUJV_ECOLI	447	YABD_BACSU	160	YBF5_YEAST	78	new ACR
S	HIN1220		88							
O	HIN1221	trxA	71							
C	HIN1222	yJae	107	A32956	341	ANATRXA_1	337	THIO_EMENI	98	thioredoxin
E	HIN1223		331	PBU17055_53	551	PADUDH_3	536	YIH4_YEAST	184	dehydrogenase
E	HIN1224	thrc	381	MU15183_6	533	MU15183_6	533	ATHOBL_1	414	cyathionine gamma-synthas
E	HIN1225	thrb	425	THRC_SERMA	1368	THRC_CONGL	230	S49036	139	threonine synthase
E	HIN1226	thra	314	KHSE_SERMA	804	KHSE_PREDI	174	KHSE_YEAST	73	homoserine kinase
S	HIN1227	yggS	815	AKIH_SERMA	2563	AK2_BACSU	276	AK_YEAST	225	aspartokinase/homoserine de
S	HIN1228	yhad	237	ECU28377_49	365			YBD6_YEAST	104	new ACR
R	HIN1229		378	YXAA_BACSU	1107	YXAA_BACSU	1107			new BCR
R	HIN1230	yaeg	419	ECU29579_37	106	YXGC_BACSU	96	B44805	79	permease
R	HIN1231		368	YABG_ECOLI	187	S39972	93			
R	HIN1232		106	APRABD_3	205	GMPY_BACSU	64			membrane protein
			56	ECU29579_32	111					transcription regulator (on

R HIN1233	251	ECPMC7A_4	124	U00015_16	91	SCPDR4_1	108	SAM-dependent methyltransferase:
S HIN1234	191							
P HIN1235	294	NM4446FBP_1	1029					periplasmic iron-binding protein
P HIN1236	473	SPUB_SEBMA	444	CYST_SYMP7	114			iron permease
E HIN1237	356	POTA_ECOLI	373	MLU01580_38	322	MDR2_CRIGR	117	transport ATPase
S HIN1238	131							
S HIN1239	146							
E HIN1240	377	DAPE_ECOLI	1091	S48588	110	YB9X_YEAST	101	succinyl-diaminopimelate dehydrogenase
O HIN1241	114	YFEB_ECOLI	246	YRUB_CLOFA	47			glutaredoxin-like protein (chaperone, HS90 family)
O HIN1242	631	HRPG_ECOLI	1598	BACGR72_27	332	S49340	306	new ACR
G HIN1243	279	CWVPH7	350	LMU017284_3	82	MTU019363_3	74	signal recognition particle
N HIN1244	462	SRS4_ECOLI	1848	SRS4_BACU	970	SRS4_ARATH	535	controls glucose repression
R HIN1245	403	SHTLYCA_2	138	SHTLYCA_2	138	SNF4_YEAST	69	
S HIN1246	297	YUJP_ECOLI	427					
S HIN1247	113							
J HIN1248	seers							seryl-tRNA synthetase
O HIN1249	gst	SYS_ECOLI	919	SYS_BACU	652	YSBYC	332	glutathione S-transferase
O HIN1250	209	S42468	123	STCPRT_3	81	S42468	123	is element
R HIN1251	98	LJU09588_1	88	LJU09588_1	68			hemolysin
P HIN1252	744	NM018558_1	113					N6-adenine-specific DNA methylase
L HIN1253	545	YWBD_BACU	122	YWBD_BACU	122	YN11_METTL	61	
M HIN1254	205							
M HIN1255	270	ECU29581_27	365	CPVARS_1	63			lytic transglycosylase mltA
R HIN1256	261	ECU29581_26	691	HNSA_AKASP	138	YK07_YEAST	163	FAD/NAD-utilizing enzyme
R HIN1257	337	TPU16363_1	83	TPU16363_1	83			adhesin
E HIN1258	168	POTR_SALTY	opt11.1					membrane protein
M HIN1259	453	ECUW93_146	1721	MURE_BACU	100			acetylmutamoyl-peptide ligase
E HIN1260	396	METC_ECOLI	1395	MLU01583_6	154	METC_YEAST	377	cytoplasmic beta-lyase
G HIN1261	185	ECODGA_2	662	BACPGS1A_1	154	PIS_YEAST	77	phosphatidylglycerophosphate
R HIN1262	176	STPPAG_1	234	MC83_1	101	STPPAG_1	234	inorganic pyrophosphatase
R HIN1263	438	YUCD_ECOLI	840					membrane protein
E HIN1264	328	YAGC_ECOLI	857	MLU01580_38	565	TAP2_RAT	113	transport ATPase
P HIN1265	550	S42804	145	RBSX_BACU	145			sulfate permease
F HIN1266	346	NM4446BP_1	69	KPPR_SYNG	63			iron-binding periplasmic protein
F HIN1267	213	URK_ECOLI	738	SCPACAS_4	120	MUSUKT_1	203	uridine kinase
S HIN1268	195	DCU_ECOLI	774		57	DCU_DESAM	95	deoxycytidine deaminase
S HIN1269	391							
R HIN1270	396	YDEA_ECOLI	356	CMLR_STRLI	209	SC9582X_14	91	permease
L HIN1271	504	U00021_5	336	U00021_5	336	MSL1_YEAST	149	Grp94, duplicated Grp94
G HIN1272	256	DP3E_ECOLI	444	DP3A_BACU	141			DNA polymerase III epsilon
R HIN1273	154	RNH_SALTY	554	MSU02015_1	301	CHKESTFL25_	184	Ribonuclease H
G HIN1274	359	S34263	86					outer membrane protein
G HIN1275	381	NAGA_ECOLI	592	URE1_BACB	74	NAGA_CAEEL	96	N-acetylglucosamine-6-phosphate
M HIN1276	270	NAGB_ECOLI	1053	MO061_1	178	HUMORFK1E	829	glucosamine-6-phosphate deaminase
G HIN1277	293	WZECN	227	DAPA_BRETA	184	PDP2HDS_1	92	N-acetylneuraminate lyase
G HIN1278	299	YNGB_CLOPE	285	STCLOPE	285	GPAAT_HUMAN	78	aminotransferase
S HIN1279	300	BCOUW67_151	449	GLK_STICO	215			sugar kinase
G HIN1280	228	BCOUW67_152	669					
	329	YTAO_ECOLI	286					C4-dicarboxylate-binding protein

R	HINI1281	633	VIAN_ECOLI	679	GNTP_BACSU	77	-	integrated membrane protein
G	HINI1282	379	YJHT_ECOLI	619	CPNANH_3	161	LPSCRJUN_1	keich domain-containing pro
S	HINI1283	63	XCB7_PSEDE	82	-	-	-	-
E	HINI1284	295	HFIC_ECOLI	502	-	-	BAN7_HUMAN	membrane protease subunit
Z	HINI1285	410	HFIC_ECOLI	502	-	-	BAN7_HUMAN	membrane protease subunit
I	HINI1286	235	LP14_BACSU	948	-	55	-	anaerobic C4-dicarboxylate )
G	HINI1287	443	DCUB_ECOLI	55	LP14_BACSU	208	ACP GRYPH	acyl carrier protein
I	HINI1288	76	AVEC	633	SAU03114_1	62	-	3-oxoacyl-[acyl-carrier pro
I	HINI1289	242	FABG_ECOLI	302	ACP ANMVA	208	FABG_ARATH	[acyl-carrier-protein] S-ma
I	HINI1290	312	B41856	913	BA72_EURSP	304	WA_EMENI	3-oxoacyl-[acyl-carrier-pro
I	HINI1291	316	FABH_ECOLI	780	BACENTR_1	303	ATHRA5111_1	ribosomal protein l32
U	HINI1292	56	R5BC02	639	STWPA8_2	326	-	-
S	HINI1293	174	YCED_ECOLI	138	DEIRPMF_1	77	-	-
I	HINI1294	290	DPSD_ECOLI	499	S38907	135	CEH0361_2	phosphatidylserine decarbox
O	HINI1295	456	GSHR_ECOLI	733	S41386	561	RDHTU	glutathione reductase
M	HINI1296	199	YAJG_ECOLI	655	-	-	-	lipoprotein
M	HINI1297	103	VANOROL_1	87	-	-	YAB6_YEAST	murein gene regulator
C	HINI1298	358	VANOROL_2	263	-	-	-	NAD:ubiquinol oxidoreductas
C	HINI1299	73	VANOROL_2	621	-	-	-	NADH:ubiquinone oxidoreduct
C	HINI1300	411	VANOROL_3	313	-	-	-	NADH:ubiquinone oxidoreduct
C	HINI1301	411	VIB1382A_1	1320	-	-	-	NADH:ubiquinone oxidoreduct
C	HINI1302	244	VANOROL_5	322	-	-	-	NADH:ubiquinone oxidoreduct
C	HINI1303	84	VANOROL_5	289	-	-	-	NADH:ubiquinone oxidoreduct
C	HINI1304	123	VANOROL_5	463	-	-	-	NADH:ubiquinone oxidoreduct
C	HINI1305	198	VIBNOR36_3	854	-	-	-	NADH:ubiquinone oxidoreduct
R	HINI1306	411	VIBNOR36_4	1776	-	-	NIA_VOLCA	Na+-translocating NADH-guin
R	HINI1307	346	YOJK_ECOLI	285	-	-	-	reductase subunit
R	HINI1308	86	-	-	-	-	-	-
S	HINI1309	418	YCFB_ECOLI	534	GUAA_BACSU	73	YCS5_YEAST	ATP-utilizing enzyme
S	HINI1310	244	YFII_ECOLI	339	YORW_CITAB	150	-	new BCR
F	HINI1311	324	YFII_ECOLI	1114	MGU02214_1	98	S50972	pseudou synthetase
S	HINI1312	262	YPIV_PSEAE	361	-	-	-	-
C	HINI1313	160	-	-	-	-	-	-
C	HINI1314	246	PFLA	1030	-	-	-	formate acetyltransferase-a
C	HINI1315	772	FOCA_ECOLI	2487	-	-	-	formate lyase
G	HINI1316	284	YADF_ECOLI	791	YWCJ_BACSU	127	YHA8_YEAST	formate transporter (formate
E	HINI1317	313	YADF_ECOLI	359	GLK_STRCO	158	-	sugar kinase/repressor
R	HINI1318	481	YEIG_ECOLI	615	BSBGJUC2_1	294	CRNA_EMENI	amino acid permease
R	HINI1319	275	YEIG_ECOLI	665	CSP1_CORGL	104	ESTD_HUMAN	esterase
R	HINI1320	378	ECGPH_1	1697	ADH_CIOBE	134	ADHX_MYXGL	glutathione-dependent forma
R	HINI1321	135	YYAN_BACSU	178	YYAN_BACSU	178	-	transcription regulator
R	HINI1322	283	YIGT_ECOLI	205	YU0017_2	102	-	membrane protein, coiled co
R	HINI1323	256	YIGU_ECOLI	845	YCBT_BACSU	190	-	integral membrane protein
E	HINI1324	449	A33504	1614	DHE2_PORGI	857	DHE4_GIALA	glutamate dehydrogenase
P	HINI1325	146	FUR_ECOLI	446	-	-	-	ferric uptake regulation pr
R	HINI1326	174	A37319	743	S04600	336	YSANNDPHCP_1	flavodoxin
C	HINI1327	287	YBFF	116	UT7036_3	98	CEIK02F3_2	dihydrolipicamide acetyltran
I	HINI1328	197	SEGA_ECOLI	329	-	-	-	negative modulator of repli
H	HINI1328	452	MEWE_SALTY	470	JX0340	117	PQ0771	o-succinylbenzoate-coenzyme

R	HINI329	yJep	1111	YJEP_ECOLI	650	-	-	-	colled coli domain-containin	
E	HINI330	aroc	357	AROC_VIBAN	741	AROC_SYNW3	524	AROC_YEAST	492	chormate synthase
M	HINI331	mePA	286	MEPA_ECOLI	670	-	-	-	mutrein endopeptidase	
R	HINI332	yfCA	255	YFCA_ECOLI	703	U00011_29	111	-	permease	
M	HINI333	mebB	318	MSBB_ECOLI	633	-	-	-	multicopy suppressor of htrI	
H	HINI334	seID	346	SELD_ECOLI	1224	YDXA_BACSU	59	PUR2_CHICK	73	selenium metabolism protein
U	HINI335	IPIS	116	S37176	530	RI19_BACST	329	HUMORF04_1	93	ribosomal protein l19
J	HINI336	trmd	246	TRMD_SERMA	1107	-	-	-	-	tRNA (guanine-N1)-methyltra
S	HINI337	yfJA	178	YFJA_ECOLI	660	-	-	-	-	-
J	HINI338	xpSP	82	RS16_ECOLI	305	RS16_BACSU	168	U3335_4	98	30S ribosomal protein S16
E	HINI339	-	257	-	-	-	-	-	-	-
E	HINI340	arOK	603	SNTD_HUMAN	151	A47026	68	SNTD_HUMAN	151	5'-nucleotidase
E	HINI341	arOB	180	ECOUW67_314	659	BSAR01_1	154	AR01_EMENT	110	shikimate kinase
E	HINI342	dam	362	AROB_ECOLI	1083	AROB_MYCTU	413	AR01_EMENT	335	3-dehydroquinate synthase
L	HINI343	pgpB	286	S47099	520	LUU16027_1	156	-	-	site-specific DNA-methyltra
I	HINI344	tlbA	241	PGPB_ECOLI	210	S32217	82	-	-	phosphatidyglycerophosphat
R	HINI345	prlB	224	GCH2_ECOLI	587	GCH2_BACSU	532	PGGTPCHUS_1	298	GRP cyclohydrolase II
E	HINI346	-	514	OPPA_SALTY	220	OPPA_BACSU	171	-	-	oligo-peptide binding prote
E	HINI347	prIC	681	OPDA_SALTY	2531	S49150	54	PRTD_YEAST	494	oligopeptidase (Zn-dependen
E	HINI348	hsdm	99	TLM1_ECOLI	294	MYCGTX_5	75	-	-	hsdm (pseudogene ?)
L	HINI349	-	385	S34396	148	-	-	-	-	hsds restriction endonucleas
S	HINI350	-	176	HTU32737_4	86	-	-	-	-	-
I	HINI351	-	1027	TLR1_ECOLI	2131	MYCGTX_4	197	-	-	type I restriction enzyme R
S	HINI352	-	213	S68137_1	954	-	-	-	-	transcription regulator, rev
C	HINI353	arCB	237	ECOUW67_139	188	PBU17609_2	99	SKN7_YEAST	98	aerobic respiration control
S	HINI354	-	325	ECOUW67_139	417	A41860	117	A48246	228	-
H	HINI355	-	196	-	-	-	-	-	-	-
F	HINI356	blrA	302	pdb1 IBA	213	BSU20445_1	117	HUMECCL_1	73	bifunctional protein: biotin
R	HINI357	guab	488	DEECIP	2031	SFUD2056_1	746	IMP2_HUMAN	542	IMP dehydrogenase
R	HINI358	-	164	IMP_ECOLI	543	SFUD2056_1	247	TRCIMPDH_1	112	splined N-terminus of Guab
F	HINI359	guaa	523	GUAA_ECOLI	1652	GUAA_BACSU	551	S45481	589	GMP synthetase
R	HINI360	-	258	RARD_ECOLI	99	YVFM_BACSU	63	-	-	membrane protein
R	HINI361	-	172	RARD_ECOLI	101	YVFM_BACSU	57	-	-	membrane protein
R	HINI362	-	168	S52279	205	IACR_LACIA	64	-	-	transcription regulator
P	HINI363	nhaA	400	S40541	942	-	-	-	-	Na+/H+ antiporter
E	HINI364	trnQ	436	BRA2_PSEAE	250	-	-	-	-	branched chain amino acid t:
E	HINI365	yfch	155	ECOUW67_150	146	-	-	-	-	-
S	HINI366	-	124	-	-	-	-	-	-	-
L	HINI367	pmp	709	PMP_ECOLI	2734	SAU19858_1	488	JC4026	159	polynucleotide phosphorylas
U	HINI368	ybbM	314	YHBM_ECOLI	616	PQ0180	89	HSU19721_1	92	peroxisomal targeting signa
J	HINI369	dead	613	ECOUW67_92	1474	YXIN_BACSU	585	YN21_CAEBL	533	rRNA (?) helicase
F	HINI370	yfhd	462	YFHD_ECOLI	886	-	-	-	-	lytic transglycosylase
S	HINI371	yhdL	69	YHDL_ECOLI	162	-	-	-	-	-
P	HINI372	arsG	116	ARSG_ECOLI	115	YGL1_STEVR	82	-	-	arsenate reductase
R	HINI373	-	349	YHHT_ECOLI	87	YCT2_BACFI	86	-	-	permease
N	HINI374	secF	325	SECF_ECOLI	585	S52166	200	-	-	protein-export membrane pro
N	HINI375	secD	616	SECD_ECOLI	972	SECD_MYCLE	188	-	-	protein-export membrane pro
S	HINI376	yajC	97	YAJC_ECOLI	217	-	-	-	-	-

S	HINI1377	yeed	73	YEED_ECOLI	80	-	-	-	azurin-like protein
R	HINI1378		172	NGAZURIN	306	-	-	-	azurin-like protein
J	HINI1379	tgt	182	C38530	1623	-	-	-	azurin-like protein
J	HINI1380	quea	363	QUEA_ECOLI	531	-	-	-	azurin-like protein
S	HINI1381		148						azurin-like protein
R	HINI1382		1409	NMIGA027_1	585	-	-	-	azurin-like protein
L	HINI1383	uvrA	943	UVRA_ECOLI	4064	SSGEMM_1	85	S51848	azurin-like protein
L	HINI1384	ssb	168	JN0632	404	UVRA_MICU	1024	STEE_YEAST	azurin-like protein
P	HINI1385	tonb	270	S14959	152	SSB_BACSU	134	SSB_HUMAN	azurin-like protein
N	HINI1386	exbd	147	EXBD_ECOLI	71	-	-	-	azurin-like protein
N	HINI1387	exbb	150	EXBB_PSEPU	80	YXND_BACSU	53	-	azurin-like protein
Z	HINI1388	bcp	155	BCP_ECOLI	525	S52934	80	PFU14189_1	azurin-like protein
L	HINI1389	dapa	298	DAPA_ECOLI	897	DAPA_BACSU	397	ZMDHPS_1	azurin-like protein
R	HINI1390		215	NLPB_ECOLI	70	C45789	70	-	azurin-like protein
L	HINI1391	yfia	107	QSECPA	348	YVVD_BACSU	65	-	azurin-like protein
S	HINI1392	rfaJ	224	NGU14554_4	244	BSYIS91C_3	83	CEP48B3_4	azurin-like protein
R	HINI1393	ygvv	195	ECU28377_52	574	U00014_4	198	CEL2C95_1	azurin-like protein
R	HINI1394		242						azurin-like protein
M	HINI1395	rfaQ	347	A48488	260	-	-	-	azurin-like protein
H	HINI1396		723	HBMR_YEREN	252	-	-	-	azurin-like protein
R	HINI1397		565	RLU23040_2	72	MU15180_36	68	-	azurin-like protein
H	HINI1398		905	HTU08349_1	1893	-	-	-	azurin-like protein
H	HINI1399	ygiG	118	ECU28379_4	385	YACE_BACSU	140	FAS_PNECA	azurin-like protein
R	HINI1400	ygiH	199	YGIH_ECOLI	765	-	-	-	azurin-like protein
P	HINI1401	narQ	567	A46162	388	BACDEGSU_1	99	MUSSPT_1	azurin-like protein
M	HINI1402	murB	341	MURB_SALTY	1077	YLXC_BACSU	137	-	azurin-like protein
L	HINI1403	rpoH	281	RP32_ECOLI	766	HRDC_STRCO	162	-	azurin-like protein
O	HINI1404	yoH	310	YOHI_ECOLI	1098	VACF_BACSU	124	YQ12_CAEEL	azurin-like protein
C	HINI1405	yabH	288	YABH_ECOLI	405	S41948	91	NPU1_YEAST	azurin-like protein
F	HINI1406	pyrE	213	ECOUW2_8	782	CAU15277_3	88	CPCURA5JB_1	azurin-like protein
J	HINI1407	rph	238	RNPH_ECOLI	1315	SYOPSREGT_	402	SCG7914_1	azurin-like protein
U	HINI1408	glxX	480	SYE_ECOLI	1315	-	-	-	azurin-like protein
R	HINI1409		551						azurin-like protein
S	HINI1410	yihY	269	YIHV_ECOLI	630	U00022_27	76	-	azurin-like protein
R	HINI1411	yichJ	161	YICH_SRIPL	124	S47149	82	-	azurin-like protein
S	HINI1412	yilM	220	YIIM_ECOLI	187	-	-	-	azurin-like protein
F	HINI1413	uop	259	S05491	939	SPSC_BACSU	65	MUSURPH_1	azurin-like protein
C	HINI1414	yhJ	438	YHJ_ECOLI	849	SCMGTP4A_1	248	ACV5_PENCH	azurin-like protein
H	HINI1415	yfbB	247	YFBB_ECOLI	169	ACVS_NOCIA	79	ILVY_YEAST	azurin-like protein
H	HINI1416	menD	568	MEMD_ECOLI	598	MEMD_BACSU	235	TRPE_YEAST	azurin-like protein
H	HINI1417	menP	430	ECMANPBN_1	309	ICSM_BACSU	124	-	azurin-like protein
S	HINI1418		139						azurin-like protein
F	HINI1419		402	AAT_BACSP	342	AAT_BACSP	342	ATVY_TRYCR	azurin-like protein
E	HINI1420	mtx	418	MTR_ECOLI	666	BSFTSAAZ_1	62	YB09_YEAST	azurin-like protein
E	HINI1421	sdac	455	SDHL_ECOLI	1257	-	-	-	azurin-like protein
E	HINI1422		412	SDAC_ECOLI	589	-	-	-	azurin-like protein
P	HINI1423		731	S49521	649	S49521	649	S43793	azurin-like protein
N	HINI1424		68	ATU1_YEAST	95	EHOCFAVZ_3	61	ATU1_YEAST	azurin-like protein

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N	HINI1425	68	ATU1_YEAST	96	EHCOPIAZ_3	60	ATU1_YEAST	96	mercury scavenger protein
R	HINI1426	128	MERR_BACSR	188	MERR_BACSR	188	-	-	transcription regulator
E	HINI1427	105	A23081	474	-	-	-	-	Met repressor
N	HINI1428	420	RHO_ECOLI	1816	RHO_BORBU	939	-	-	transcription terminator, R
N	HINI1429	220	ECU28377_70	171	-	-	-	-	prepilin leader peptidase
N	HINI1430	406	AHU20255_3	320	CMG2_BACSU	89	-	-	transport protein
N	HINI1431	464	AHU20255_2	782	B3038	291	-	-	transport protein (pilin bi
N	HINI1432	149	PPDD_ECOLI	210	PPDA_CLOHE	85	-	-	prepilin
E	HINI1433	ampd	AMPD_ECOLI	462	SHITLYCA_2	234	-	-	signalling protein
E	HINI1434	289	SHITLYCA_2	234	SHITLYCA_2	234	-	-	cystathionine beta-synthase
E	HINI1435	522	INT_ECOLI	367	-	-	-	-	apolipoprotein N-acyltransf
E	HINI1436	245	ECU28377_44	661	U00016_17	98	-	-	nucleosidase
S	HINI1437	186	ECU28377_46	191	-	-	-	-	-
S	HINI1438	56	-	-	-	-	-	-	-
S	HINI1439	139	ECU28377_47	501	-	-	-	-	-
S	HINI1440	302	YAD_ECOLI	604	-	-	-	-	-
E	HINI1441	271	VIBPROCY_3	607	PROH_BACSU	142	PFU27806_1	125	pyrrolidine-5-carboxylate red
R	HINI1442	388	S49295	194	YMBF_BACSU	106	YB14_YEAST	65	permease
L	HINI1443	xerD	XERD_ECOLI	1081	CODV_BACSU	272	-	-	integrase/recombinase
L	HINI1444	rvbB	RVB_ECOLI	1374	RVB_MYCLE	921	PFACDCATP_1	92	Holliday junction DNA helic
L	HINI1445	rvuA	A32358	500	RVUA_MYCLE	193	-	-	Holliday junction DNA helic
L	HINI1446	rvuC	D38113	631	RVUC_MYCLE	135	-	-	-
E	HINI1447	yebC	YEB_C_ECOLI	1004	U00011_23	196	-	-	-
E	HINI1448	ncpA	NTPA_ECOLI	378	MOTT_STRAM	78	-	-	-
U	HINI1449	asps	SYD_ECOLI	2320	SYD_MYCLE	633	SYDM_YEAST	253	dapt pyrophosphohydrolyase
S	HINI1450	172	SABAGBA	158	SABAGBA	158	-	-	aspartyl-tRNA synthetase
L	HINI1451	241	CM4T_STRPE	80	CM4T_STRPE	80	YB9H_YEAST	60	methyltransferase
L	HINI1452	78	C49205	84	-	-	-	-	virulence plasmid protein
L	HINI1453	134	B49205	129	-	-	-	-	virulence-associated protei
R	HINI1454	135	VP006949_6	522	YWBC_BACSU	100	SC9571X_14	138	lactoylglycerol kinase
L	HINI1455	420	RNT_ECOLI	702	MPU06833_1	94	-	-	ribonuclease T
R	HINI1456	259	VP006949_1	390	NHAC_BACFI	80	-	-	permease
U	HINI1457	efp	S34443	749	ANACCB_1	364	HYPU_SULAC	67	elongation factor P
R	HINI1458	338	YJER_ECOLI	863	-	-	MTDNAOMA_2	42	ferredoxin-like protein
S	HINI1459	431	YTFB_ECOLI	119	-	-	-	-	-
R	HINI1460	134	-	-	-	-	-	-	-
L	HINI1461	reco	RECO_ECOLI	363	YOXN_BACSU	98	-	-	opacity-associated membrane
L	HINI1462	YCga	ECU29580_10	771	KSGA_BACSU	72	RNC1_YEAST	87	RNA repair protein
U	HINI1463	rela	VSU13765_2	1239	U00011_5	446	-	-	SAN-dependent methyltransfe
H	HINI1464	dgka	KIRCDG	274	BSU2177_6	105	-	-	pppG synthetase I
I	HINI1465	mog	MOG_ECOLI	801	S05373	60	GEPR_RAT	218	diacylglycerol kinase
P	HINI1466	glnB	GLNB_ECOLI	476	A39696	366	MIOF_3	153	molybdoprotein biosynthesis
R	HINI1467	yhtT	S47693	432	YCT2_BACFI	90	-	-	nitrogen regulatory protein
L	HINI1468	prfA	A35505	1475	MFD_BACSU	80	HCA5_YEAST	71	permease
R	HINI1469	Y9GH	ECU28377_58	688	S44970	62	-	-	primosome helicase
S	HINI1470	Y9GL	ECU28377_57	372	-	-	-	-	SAN-dependent methyltransfe
C	HINI1471	Y9JG	Y9JG_ECOLI	224	CAU15277_2	67	PER_ENTHI	58	ferredoxin
S	HINI1472	Y9JF	Y9JF_ECOLI	170	-	-	-	-	-

C	HINI473	yojC	819	YOJC_ECOLI	3307	NABE_STNP7	210	-	nitrate reductase
C	HINI474	yojB	279	YOJB_ECOLI	736	S40170	70	SC652X_3	ferredoxin-like protein
C	HINI475	yej2	287	YEJ2_ECOLI	832	PHFI_CLOFA	67	FER_ENTH1	ferredoxin
C	HINI476	yejY	150	YEJY_ECOLI	294	-	-	-	cytochrome c
C	HINI477	yejX	200	YEJX_ECOLI	468	-	-	-	cytochrome c
F	HINI478	adk	214	KAD_SALT1	830	KAD_BACSE	353	J01944	adenylosuccinate kinase
F	HINI479	amps	425	AMPE_ECOLI	349	COMP_BACSU	77	CET26C5_3	signal transducer (sensor)
G	HINI480	galE	338	GALF_ERWMM	1151	GALF_STRRR	194	GALF_RAT	UDP-glucose 4-epimerase
S	HINI481		231						
E	HINI482		240	PROV_ECOLI	175	BACOPA_4	173	MDR4_DROME	transport ATPase
R	HINI483		240	YZEB_BACSU	293	YZEB_BACSU	293	NAH4_RAT	permease
H	HINI484		316	NMT1_SCHRO	197	YZEB_BACSU	108	NMT1_SCHPO	pyrimidine (thiamine ?) pre
K	HINI485		215	TEBA_BACSU	104	TEBA_BACSU	64	YCRO_YEAST	transcription activator
R	HINI486		281	SYCMNTABC_3	762	SYCMNTABC_3	762	-	membrane protein
R	HINI487		272	SYCMNTABC_3	648	SYCMNTABC_3	648	-	membrane protein
R	HINI488		306	SYCMNTABC_2	773	SYCMNTABC_2	773	ABC2_MOUSE	transport ATPase
R	HINI489		293	SYCMNTABC_1	890	SYCMNTABC_1	890	-	peptidase
M	HINI490	pbpG	292	PBP7_ECOLI	220	DABG_BACSU	111	-	penicillin-binding protein,
S	HINI491	yFgB	390	YFGB_ECOLI	1540	-	-	-	new ACR
S	HINI492		179	CELK001D1F	87	-	-	CELK001D1F	87
S	HINI493	yFgA	303	YFGA_ECOLI	102	-	-	-	essential in E.coli
R	HINI494	gcpeE	368	GCPE_ECOLI	1533	-	-	-	histidine--tRNA synthetase
J	HINI495	hiss	423	SYECH	1197	SYH_STREQ	476	SC9367_13	colicin
M	HINI496		204	CEA1_ECOLI	79	-	-	-	
S	HINI497	yfhJ	64	YFHJ_ECOLI	264	-	-	-	
C	HINI498	fdx	113	JC1110	408	THCC_RHOSO	59	ADX_CHICK	ferredoxin
C	HINI499	hscA	619	AS3488	1074	DNAK_CHLPH	556	GR78_SCHPO	chaperone
O	HINI500	ybfG	228	YBFG_ECOLI	229	-	-	-	ferredoxin
O	HINI501	yfheE	174	YFHE_ECOLI	172	-	-	-	
R	HINI502	yfhF	107	YFHF_ECOLI	359	-	-	YJ01_YEAST	72
R	HINI503		151	NITU_ELEBN	141	NITU_ANASP	121	-	109
K	HINI504		406	NFS1_YEAST	1162	NIFS_BACSU	373	NFS1_YEAST	1162
S	HINI505	yjeb	240	RRP2_DESVH	194	LACIPAPAP_2	92	-	-
J	HINI506	laet	151	IASIT_SERVA	118	YACO_BACSU	65	-	-
M	HINI507	pal	153	PMU16849_1	561	TRPTP5X_1	76	-	-
M	HINI508		427	JV0058	732	-	-	-	-
M	HINI509	tolA	372	TOIA_ECOLI	267	-	-	-	-
M	HINI510	tolR	139	TOIR_ECOLI	749	-	-	-	-
M	HINI511	tolQ	228	TOIQ_ECOLI	915	-	-	-	-
S	HINI512	ybgC	136	YBGC_ECOLI	239	-	-	-	-
L	HINI513	ding	640	DING_ECOLI	175	-	-	-	-
M	HINI514		236	YGAD_ECOLI	143	-	-	-	-
M	HINI515	sip	183	SIP_ECOLI	112	-	-	-	-
I	HINI516	faad	562	LCPA_ECOLI	1054	S49518	175	CELPA1C3_7	152
L	HINI517	rnd	399	RND_ECOLI	490	MLU15181_26	92	CEC1A4_4	89
R	HINI518		182						
R	HINI519		245						
R	HINI520	ychF	363	PIIC2_AGRTU	76	JC04001	64	CF909B_2	62
R	HINI520		245						
R	HINI520		245						
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R	HINI520		245						
R	HINI520		245						



J HIN1511	pth	194	PTH_ECOLI	667	SP5C_BACSU	194	YHY9_YEAST	81	peptidyl-L-trna hydrolase
S HIN1522	yefD	102	YCFD_ECOLI	-	BACGMTZ_21	59	-	-	-
S HIN1523	xseA	439	EX7L_ECOLI	1253	MUTX_STREPN	70	YSA1_YEAST	85	exonuclease VII, large subu
R HIN1524	rdsA	217	ECU28377_13	388	Y168_SYMP6	89	MR11_YEAST	44	NTP pyrophosphohydrolase (M
R HIN1525	icc	274	ICC_ECOLI	772	-	-	-	-	phosphoesterase
R HIN1526	y11S	95	Y11S_ECOLI	91	-	-	-	-	-
I HIN1527	fadL	459	FADL_ECOLI	370	-	-	-	-	outer membrane protein (fat
L HIN1528	ogt	190	OGD3_BACSU	263	ADAB_BACSU	263	MGMT_YEAST	206	methylated-DNA-protein-cys
L HIN1529	mutH	223	MUTH_ECOLI	704	TS33_STRAU	60	-	-	DNA mismatch repair protein
R HIN1530	accA	430	YAC4_BACSU	158	YAC4_BACSU	158	HSU10860_1	51	ATP-utilizing enzyme
G HIN1531	yebI	288	YEBI_SALTY	235	YMDB_BACSU	61	YEC9_YEAST	159	sugar kinase
I HIN1532	accA	315	A43452	1157	BACPK_1	834	S49909	688	acetyl-CoA carboxylase
P HIN1533	yebI	261	YEBI_ECOLI	586	P29K_STRGC	219	-	-	integral membrane protein
R HIN1534	yebA	288	YEBF_ECOLI	155	LU009553_1	166	-	-	transport ATPase
R HIN1535	tyrB	478	TYRB_ECOLI	284	SVOCGB_10	158	TAP1_HUMAN	133	membrane metalloendopeptida
R HIN1536	htg	318	TYRB_ECOLI	376	CLOCOR_1	282	-	-	transcriptional regulator, i
R HIN1537	yecC	91	S26832	351	MSU02214_1	196	SPAC18B11_2	125	pseudonuclease E
J HIN1540	rne	322	YCEC_ECOLI	1071	SPU23762_2	76	DNAJ_METWA	58	ribonuclease
M HIN1541	rne	951	RNE_ECOLI	1079	-	-	-	-	opacity protein (membrane)
H HIN1542	OP67_NERGO	70	OP67_NERGO	238	YMBJ_BACSU	355	TH14_SCHPO	191	thymine biosynthesis enzym
G HIN1543	YMBJ_BACSU	265	YMBJ_BACSU	355	YMBJ_BACSU	183	SI4885	194	sugar kinase
G HIN1544	YMBK_BACSU	226	YMBK_BACSU	183	YMBK_BACSU	183	TH16_YEAST	168	thiamin-phosphate pyrophosp
R HIN1545	YHJF_ECOLI	434	YHJF_ECOLI	736	E47031	247	RNCATTRA_1	82	permease
R HIN1546	yhbU	460	ECOUW67_88	170	PRTC_PORGI	118	-	-	protease
S HIN1547	-	99	-	-	-	-	-	-	-
J HIN1548	srmB	439	SRMB_ECOLI	1418	XYIN_BACSU	269	S42639	477	RNA helicase
I HIN1549	yfjC	240	YFJC_ECOLI	403	BACGMTZ_20	61	CEIC18A3_5	66	adenine-specific DNA methyl
J HIN1550	yfjF	351	YFIF_ECOLI	461	-	-	-	-	rRNA methylase
I HIN1551	psaA	455	PSS_ECOLI	589	BSDNA320D_6	72	SCPELIGN_1	68	CDD-diacylglycerol--serine
I HIN1552	fadsr	241	S01288	666	S33420	86	-	-	fatty acid metabolism regul
P HIN1553	nhab	522	NHAB_ECOLI	1203	MSG4_SMP_1	94	-	-	NA(+)/(H(+)) antiporter
E HIN1554	dsbB	177	A48288	242	-	-	-	-	disulfide bond formation pr
E HIN1555	glms	610	ECOUW82_93	1555	U00020_16	343	U00932_1	371	glutamine amidotransferase
L HIN1556	hupa	136	DBH_VIBPR	352	DBH_BACST	291	DBH_CRYPH	169	DNA-binding protein
L HIN1557	yjaG	196	YJAG_ECOLI	439	-	-	-	-	-
R HIN1558	yjad	264	YJAD_ECOLI	270	MUTX_STREPN	70	80DP_HUMAN	68	pyrophosphohydrolase (mutr
R HIN1559	yhgI	198	ECOUW67_339	720	S49995	63	SCX112_1	66	thioredoxin
F HIN1560	yphH	229	ECOUW67_338	321	JN0886	71	PUR1_CHICK	89	phosphoribosyltransferase; ;
N HIN1561	hopQ	445	ECOUW67_315	464	-	-	-	-	general secretion protein
S HIN1562	-	137	-	-	-	-	-	-	-
S HIN1563	-	173	-	-	-	-	-	-	-
S HIN1564	-	168	-	-	-	-	-	-	-
S HIN1565	mrca	265	-	-	-	-	-	-	-
M HIN1566	yhbA	864	YHB_A_ECOLI	940	DBPF_BACSU	450	-	-	-
S HIN1567	yhbR	281	YHB_R_ECOLI	678	-	-	-	-	-
S HIN1568	yhbB	121	YHB_B_ECOLI	497	YNAK_BACSU	107	-	-	-

penicillin-binding D-alany

L HIN1569	recR	200	BVECR	804	REC_BACSU	321	-	recombinational DNA repair )	
L HIN1570	topB	651	TOP3_ECOLI	927	S45077	231	TOP3_YEAST	71	topoisomerase III
L HIN1571	secG	112	SEC3_ECOLI	291	SEC3_MYCE	67	-	protein-export translocatio	
G HIN1572	fuaA	556	PYR3_XANCP	839	PYR3_BACM	399	-	fructose-phosphatase IIB comp	
G HIN1573	fukK	313	K1PF_ECOLI	710	LAC3_STAUD	129	KHK_RAT	73	1-phosphofructokinase
G HIN1574	futB	499	PTFA_ECOLI	467	J00088	208	-	fructose-phosphatase IIA/PFR c	
R HIN1575	-	178	-	-	-	-	-	virulence-associated protein	
R HIN1576	-	91	A49205	178	-	-	-	-	
S HIN1577	-	63	-	-	-	-	-	-	
M HIN1578	YfFl	432	YTFfl_ECOLI	861	SHTLYCA_2	112	CBS_HUMAN	71	hemolysin, new ACR
S HIN1579	-	174	-	-	-	-	-	-	
S HIN1580	YcfH	260	YABD_BACSU	440	YABD_BACSU	440	YBF5_YEAST	71	new ACR
L HIN1581	ho1B	327	S35523	262	BSDMAX_1	118	DMU15967_1	82	DNA-directed DNA polymerase
F HIN1582	YofG	210	YOFG_ECOLI	346	YAP_BACSU	202	KTH_YEAST	53	pyrimidine kinase
S HIN1583	YocG	347	YOCG_ECOLI	244	-	-	-	-	-
O HIN1584	surA	313	S40574	286	PRSA_BACSU	88	YPI3_DICDI	69	peptidyl-prolyl cis-trans i
F HIN1585	-	179	PYR4_BACU	299	PYR4_BACCU	299	SMHGPRT_1	85	uracil phosphoribosyltransf
R HIN1586	mazG	263	ECU29580_6	384	YABN_BACCU	297	-	-	beta-lactamase regulatory p
R HIN1587	-	291	YOF2_PASHA	152	-	-	-	-	membrane protein
R HIN1588	lon	803	LON_ECOLI	2278	LON_BACGR	1317	S42365	637	ATP-dependent protease
C HIN1589	Y9GW	383	ECU28377_53	1189	-	-	-	-	ferredoxin-like oxidase
C HIN1590	rp1A	219	S22097	400	-	-	MUSPDI_1	145	ribose 5-phosphate isomeras
C HIN1591	serA	410	DEBCPG	1279	LDHDA6_1	226	YER1_YEAST	700	phosphoglycerate dehydrogen
S HIN1592	YgfZ	280	ECU28375_48	190	MLU15182_13	80	-	-	-
S HIN1593	Y4CC	287	Y1CC_ECOLI	963	-	-	-	-	-
E HIN1594	h1sg	303	HIS1_ECOLI	1061	HIS1_LACIA	136	HIS1_SCHPO	127	ATP phosphoribosyltransfera
E HIN1595	h1sg	427	ECU1HSDH_1	691	HISX_LACIA	395	HIS2_YEAST	403	histidinol dehydrogenase
E HIN1596	h1sc	367	HIS8_ECOLI	1132	HIS8_STRCO	166	HIS8_SCHPO	173	histidinol-phosphate aminot
E HIN1597	h1sh	362	HIS7_ECOLI	730	HIS7_STRCO	276	HIS7_PHYPR	270	imidazoleglycerol-phosphate
E HIN1598	h1sh	199	HIS5_SALTY	294	HIS5_LACIA	153	HIS5_YEAST	94	glutamine amidotransferase
E HIN1599	h1sa	245	HIS4_ECOLI	810	HIS4_LACIA	228	HIS5_YEAST	50	phosphoribosylformimino-5-a
E HIN1600	h1sf	258	HIS6_ECOLI	1098	HIS6_LACIA	326	HIS5_YEAST	200	cyclase (histidine biosynth
E HIN1601	h1st	221	ECORFBI_9	366	HIS2_LACIA	263	S53349	119	phosphoribosyl-AMP cyclohyd
E HIN1602	-	400	TYRP_ECOLI	407	-	-	-	-	amino acid permease
C HIN1603	atpC	142	ATPE_ECOLI	397	S37548	157	-	-	ATP synthase F1 epsilon sub
C HIN1604	atpD	457	PWECB	1970	ATPX_BACFI	1233	-	-	H+-transporting ATPase beta
C HIN1605	atpE	289	ATPG_ECOLI	676	ATPG_BACFI	338	-	-	ATP synthase F1 gamma subun
C HIN1606	atpA	513	ATPA_ECOLI	2271	ATPA_BACST	971	-	-	ATP synthase F1 alpha subun
C HIN1607	atpH	177	ATPD_ECOLI	513	ATPD_PROMO	140	-	-	ATP synthase F1 delta subun
C HIN1608	atpF	156	ECODNCE_1	492	ATPF_PROMO	198	-	-	ATP synthase F0 subunit b
C HIN1609	atpB	84	ATPD_VIBAL	270	ATPD_BACFI	131	-	-	H+-transporting ATP synthas
R HIN1610	atpB	262	ATPD_ECOLI	332	ATPD_BACFI	151	-	-	ATP synthase F0 subunit a
R HIN1611	g1db	203	G1DB_ECOLI	678	MSGDNAB_19	144	RATDHPMT_1	45	glucose-inhibited division )
S HIN1612	yhfY	125	ECOW67_306	101	-	-	-	-	-
R HIN1613	-	200	YHFE_ECOLI	117	U00015_17	96	GSI_HUMAN	70	hydrolyase (phosphatase ?)
R HIN1614	-	157	S39339	57	S39339	57	-	-	alkaline phosphatase ?
S HIN1615	YgaG	167	YgaG	415	-	-	-	-	-
R HIN1616	-	118	S47779	211	MHU01217_1	168	-	-	transposase

R	HINI1617	Yjbp	230	YUBP_ECOLI	391	-	-	-	acid phosphatase
O	HINI1618	ha1v	175	HSIV_ECOLI	518	HSIV_BACSU	307	-	proteasome-related protease
E	HINI1619	ha1v	444	PASIAFCART	1057	HSIV_BACSU	570	YB77_YEAST	ATP-dependent protease
C	HINI1620	yejA	312	POTD_ECOLI	839	STRALAKXP_1	77	SC9952X_6	spermidine/putrescine-binding
K	HINI1622	YjGN	431	YjGN_ECOLI	308	CSU23395_4	87	CELCl5812_4	NAD/PAD-utilizing oxidoreductase
G	HINI1623	rbSD	346	YjGN_ECOLI	637	-	-	-	coiled coil domain-containing
G	HINI1625	rbSA	139	RBSD_ECOLI	446	RBSD_BACSU	195	-	high affinity ribosome transposon
G	HINI1626	rbSB	493	RBSA_ECOLI	1319	RBSD_BACSU	554	ABC2_MOUSE	ribosome transport ATPase
G	HINI1626	rbSC	323	RBSB_ECOLI	1070	RBSB_BACSU	488	-	high affinity ribosome transposon
G	HINI1627	rbSK	306	RBSK_ECOLI	872	RBSB_BACSU	407	-	D-ribose-binding periplasmic
G	HINI1627	rbSK	332	RBSK_ECOLI	843	RBSK_BACSU	188	RBSK_YEAST	ribozyme
S	HINI1629	YjSR	183	ECOUW82_119	423	CLOREP_1	236	-	ribose operon repressor
H	HINI1630	menG	162	MENG_ECOLI	575	-	-	-	menaquinone biosynthesis protein
H	HINI1631	mena	308	MENA_ECOLI	655	YVAB_BACSU	159	-	menaquinone biosynthesis protein
S	HINI1632	YaeB	239	YAEB_ECOLI	648	-	-	-	tellurite resistance protein
P	HINI1633	teha	328	TEHA_ECOLI	359	-	-	-	HincII endonuclease
L	HINI1634	-	258	-	-	-	-	-	HincII methylase
L	HINI1635	-	144	BAMBAN11_1	92	YJ12_YEAST	86	-	DNA-directed RNA polymerase
L	HINI1636	TPOC	1415	RPOC_ECOLI	5134	BACBP0_1	1249	RPI1_SCHPO	DNA-directed RNA polymerase
L	HINI1637	TPOL	1343	RPOB_SALTYE	3143	RPOB_MYTE	1001	RPOB_PLAFA	DNA-directed RNA polymerase
J	HINI1638	rplA	229	RSECI	987	RL1_STTGR	573	RL1_HALMA	ribosomal protein L1
J	HINI1639	rpik	142	RSEB11	638	S39860	311	YKAE_CAEEL	50S ribosomal protein L11
F	HINI1640	deod	238	A27854	1021	MYCPHDOR_1	89	MUSURPH_1	purine-nucleoside phosphorylase
E	HINI1641	YjIM	417	YEIM_ECOLI	432	NDPC_BACSU	131	AS4892	nucleoside permease
S	HINI1642	YjJW	262	YJW_ECOLI	126	ANMOA_1	42	CEF49E2_3	ferredoxin-like protein
C	HINI1643	YjJ1	514	YJW_ECOLI	251	-	-	-	ferredoxin
M	HINI1644	-	218	-	104	YVAS_BACSU	104	-	integral membrane protein
N	HINI1645	-	356	RFAK_ECOLI	79	MYGLIX_4	74	-	ADP-heptose:lipheptosyltransferase
C	HINI1646	fba	359	ADBC2A	1410	S09283	145	PGK2_HUMAN	fructose-bisphosphate aldolase
C	HINI1647	pgk	386	TYECG	1226	PGK_BACST	220	RNS1_ARATH	phosphoglycerate kinase
L	HINI1648	rna	272	RNI_ECOLI	88	-	-	-	ribonuclease I
C	HINI1649	-	86	FER_CHRVI	232	FER2_CHILLI	191	A45620	ferredoxin
E	HINI1650	tyrP	406	FER_GRECV	741	RREUTPBC_2	64	GLTE_RABIT	lysine-specific permease
F	HINI1651	tdk	193	KITH_ECOLI	691	STRIDNDC_1	310	KITH_CHICK	thymidine kinase
C	HINI1652	YjJD	342	GCP_PSH2	1386	U00015_29	241	OR17_YEAST	sialoglycoprotease
J	HINI1653	tpsU	71	R3EC21	297	RS21_BACST	147	-	ribosomal protein S21
L	HINI1654	dnag	593	PRIM_ECOLI	1044	PRIM_BACSU	817	-	DNA primase
L	HINI1655	tpod	629	ECOU28379_14	1561	RPSA_CIOAB	377	-	RNA polymerase sigma-70 factor
E	HINI1656	aspa	475	ECOUW93_54	1397	ASPA_BACSU	957	FUWH_YEAST	aspartate ammonia-lyase
E	HINI1657	-	261	UREH_HELPY	126	BP023368_5	113	-	urease-associated protein
E	HINI1658	-	225	UREG_HELPY	736	UREG_BACSB	673	MS1_YEAST	urease-associated protein
E	HINI1659	-	246	UREF_BACSB	326	UREF_BACSB	326	-	urease accessory protein
E	HINI1660	-	185	BP029368_2	158	BP029368_2	158	-	urease accessory protein
E	HINI1661	-	572	S36028	1237	URE1_BACPA	1204	UREA_CANEN	urease alpha subunit
E	HINI1662	-	101	URE2_KLEAB	324	URE2_BACSB	313	UREA_CANEN	urease beta subunit
E	HINI1663	-	100	URE3_BACSB	351	URE3_BACSB	351	UREA_CANEN	urease gamma subunit
O	HINI1664	gros	96	ECGROS_1	423	CH10_CHLPP	173	CH10_HUMAN	GROES co-chaperonin

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O HINI1665	grol	548	YEPHSCP2_2	2029	S33213	1507	CH60_ARATH	1431	GROEL, chaperonin
U HINI1666	rplI	149	RL9_ECOLI	534	RL9_SYNY3	182	-	-	50S ribosomal protein l9
U HINI1667	rpsr	75	ECOW93_114	360	RS18_BACST	226	YEO0_YEAST	81	30S ribosomal protein S18
U HINI1668	prtb	108	O4BFCR	287	-	-	-	-	30S ribosomal protein S18
U HINI1669	rpsf	125	RS6_ECOLI	502	MSGDNAB_4	129	-	-	30S ribosomal protein S6
U HINI1670	infA	84	FILEC1	352	BACALPHA_1	272	-	-	translational initiation factor
M HINI1671	ksqA	287	KSGA_ECOLI	629	KSGA_BACSU	227	DIM1_YEAST	137	translational initiation factor
M HINI1672	-	302	NGU14554_6	188	-	-	CD2045_4	92	glycosyl transferase
F HINI1673	apah	275	APAH_ECOLI	803	-	-	RDCG_DROME	68	bis (5'-nucleosyl)-tetrphos
S HINI1674	-	207	NGAZRIN	178	-	-	-	-	-
C HINI1675	gnd	484	ECOR3_1	1170	S14628	465	DESHGC	1092	6-phosphogluconate dehydrog
C HINI1676	-	180	HUI32707_2	86	-	-	-	-	-
S HINI1677	-	79	YTRP_LACIA	85	YTRP_LACIA	85	-	-	New BCR
C HINI1678	-	163	A47563	93	ASU14553_2	78	YC13_YEAST	84	glucose-6-phosphate dehydrog
C HINI1679	zwf	494	NOSTFZOOP_3	655	NOSTFZOOP_3	655	S31337	427	glucose-6-phosphate 1-dehy
P HINI1680	cysQ	228	ECOW93_126	170	U00017_33	79	QUTG_EMENT	109	sulfite synthesis pathway p
R HINI1681	-	471	S38663	417	MU15187_34	55	MECST4_1	68	permease
R HINI1682	-	219	S38663	143	BIOY_BACSH	52	-	-	membrane protein
S HINI1683	yrfH	131	ECOW67_324	466	VABO_BACSU	102	-	-	new BCR
E HINI1684	asnC	150	ASNC_ECOLI	503	-	-	YGDH_PYRFU	162	transcription regulator
E HINI1685	asna	330	ASNA_ECOLI	1099	-	-	-	-	asparagine synthetase
R HINI1686	yphE	224	YHPE_ECOLI	328	YFGS_LACCA	92	HIS7_PHYPR	88	hydroxylase (phosphatase ?)
C HINI1687	yphF	234	ECOW67_310	928	MEU02181_1	89	STPEPTMR_1	323	pentose phosphate epimerase
L HINI1688	yphG	806	GYRB_ECOLI	2416	GYRB_BACSU	848	TOP2_CRIPA	173	DNA gyrase subunit b
L HINI1689	yphF	698	ECOW67_332	2187	RS1H_BACSU	189	JC4026	180	ribosomal protein S1 homolog
L HINI1690	greB	158	ECOW67_330	487	S48616	70	-	-	transcription elongation fac
R HINI1691	yjIC	205	YJIC_ECOLI	661	MU15180_21	88	-	-	transcriptional repressor?
M HINI1692	oxyR	301	A33145	1120	MAU18265_2	351	LKU11244_1	152	hydrogen peroxide-inducible
C HINI1693	-	241	LKU11244_1	1122	YR0B_CLOPA	74	-	-	glutaredoxin-like membrane
R HINI1694	slxX	73	SLX_X_ECOLI	173	-	-	-	-	colled coil domain-contains
O HINI1695	fkpA	241	ECOW67_271	351	MIP_CHLTR	155	TCMIP_1	231	peptidyl-prolyl cis-trans i
S HINI1696	yheN	126	ECOW67_269	504	-	-	-	-	-
S HINI1697	-	119	ECOW67_268	157	-	-	-	-	-
U HINI1698	-	119	ECOW67_268	157	-	-	-	-	-
U HINI1699	tufr	394	EJECT	1904	EFTU_BACFR	1552	EF1A_CANAL	154	translation elongation factor
U HINI1700	fusa	700	JC1424	1365	EBF3_STIRA	1027	S35701	826	translation elongation factor
U HINI1701	ipsg	156	JC1423	719	RS7_BACST	518	RS5_PODCA	71	30S ribosomal protein S7
U HINI1702	ipsl	124	R3BC12	625	RS12_SPIPL	504	RS23_HUMAN	52	30S ribosomal protein S12
R HINI1703	gidA	629	GIDA_ECOLI	2133	GIDA_BACSU	843	NEMTTSPA_1	80	glucose inhibited division